

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 9, 2005, 11:30:14 ; Search time 43 Seconds  
(without alignments)  
1203.828 Million cell updates/sec

Title: US-10-620-169-4  
Perfect score: 2958  
Sequence: 1 MPRGWAPLILLQLQGWC.....YLRQWVPPPLSSPGQAS 538

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	278	9.4	551	2 A30342	interleukin-2 rece
2	249	8.4	537	2 B46535	interleukin 2 rece
3	247.5	8.4	539	2 A35052	interleukin-2 rece
4	233	7.9	896	1 A35782	cytokine receptor
5	221.5	7.5	468	2 A45268	interleukin-9 rece
6	218.5	7.4	878	1 A40091	interleukin-3 rece
7	215	7.3	522	2 B45268	interleukin-9 rece
8	213.5	7.2	467	2 I56896	gene gfi-2 protein
9	213	7.2	508	1 ZUHUR	erythropoietin rec
10	211.5	7.2	896	2 I56563	interleukin-3 rece
11	204	6.9	897	1 A32555	cytokine receptor
12	201	6.8	507	1 A32385	erythropoietin rec
13	195	6.6	507	1 A46713	erythropoietin rec
14	193.5	6.5	825	1 A60386	interleukin-4 rece
15	189.5	6.4	810	1 A33380	interleukin-4 rece
16	171	5.8	348	2 JC7907	common cytokine re
17	168.5	5.7	635	2 A45266	MPL-P protein prec
18	168.5	5.7	800	1 S31575	interleukin-4 rece
19	168	5.7	369	2 I49280	interleukin-2 rece
20	164.5	5.6	579	2 B45266	MPL-K protein prec
21	159	5.4	831	2 J01655	prolactin receptor
22	157	5.3	625	2 S35317	hematopoietic grow
23	157	5.3	626	2 S37622	proto-oncogene - m
24	151.5	5.1	805	2 S68441	leptin receptor, s
25	151.5	5.1	892	2 S68439	leptin receptor, s
26	151.5	5.1	894	2 S68437	leptin receptor, s
27	151.5	5.1	900	2 S68440	leptin receptor, s
28	151.5	5.1	1162	2 S68438	leptin receptor, s
29	146	4.9	459	2 A34791	interleukin-7 rece

30	144	4.9	373	2 A55718	interleukin-2 rece
31	143.5	4.9	459	2 D34791	interleukin-7 rece
32	143	4.8	369	2 A42565	interleukin-2 rece
33	139.5	4.7	298	2 B34791	interleukin-7 rece
34	139	4.7	895	2 S74225	leptin receptor, i
35	139	4.7	1162	2 PC4184	leptin receptor, O
36	135.5	4.6	954	1 S68178	mixed-lineage prot
37	128.5	4.3	284	2 S27931	Env/v-mpl fusion p
38	128.5	4.3	918	2 A44257	interleukin-6 sign
39	126.5	4.3	917	2 I49699	glycoprotein 130 -
40	125	4.2	262	2 C34791	interleukin-7 rece
41	123	4.2	295	2 A44984	collagen - nematod
42	123	4.2	468	1 A41242	interleukin-6 rece
43	123	4.2	1744	2 S40991	collagen alpha 1(I)
44	122.5	4.1	420	2 S21052	interleukin-5 rece
45	121.5	4.1	2124	2 A28452	proteoglycan core

ALIGNMENTS

RESULT 1

A30342  
Interleukin-2 receptor beta chain precursor - human  
N:Alternate names: CD25 beta chain  
C:Species: Homo sapiens (man)  
C>Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 09-Jul-2004  
C:Accession: A30342  
R:Hatakeyama, M.; Tsudo, M.; Minamoto, S.; Kono, T.; Doi, T.; Miyata, T.; Miyasaka, M.;  
Science 244, 551-556, 1989  
A>Title: Interleukin-2 receptor beta-chain gene: generation of three receptor forms by  
A:Reference number: A30342; MUID:89242117; PMID:2785715  
A:Accession: A30342  
A:Molecule type: mRNA  
A:Residues: 1-551 <HAT>  
A:Cross-references: UNIPROT:P14784; GB:M26062; NID:q186322; PIDN:AAA59143.1; PID:G307048  
C:Genetics:  
A:Gene: GDB:IL2RB  
A:Cross-references: GDB:118822; OMIM:146710  
A:Map position: 22q11.2-22q13  
C:Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology  
C:Keywords: cytokine receptor; transmembrane protein  
F:1-26/Domain: signal sequence #status predicted <SIG>  
F:27-551/Product: interleukin-2 receptor beta chain #status predicted <MAT>

Query Match	9.4%	Score 278;	DB 2;	Length 551;
Best Local Similarity	26.0%	Pred. No. 4.7e-12;		
Matches 137;	Conservative 75;	Mismatches 199;	Indels 116;	Gaps 31;
QY	5	WAAPLILL--LQGW-----GCPDLVCYTDYLTQTVICILEMNLHPSTLTLTWDDQVE	56	
Db	8	WRLPLILLPLATSWASAAVNGTSQFTCFYNSRANISCV---WS-----QDG	52	
QY	57	ELKDEATSCSLH-----RSAHNAT-----HATYTCM-----DVFHFWADDFSVNITD	100	
Db	53	ALQD--TSCQVHAMPDRRRNQTCELLPVSQASWACNLILGAPDSQKLTVDIVTLRLVC	110	
QY	101	OSGNYSORCG--SFLLAESIKPAPPFNVTVF--SGQYNISWRSDYEDPAFMLKGLQY	156	
Db	111	REGVWRVMAQDFKPFENLRMAPISLOVVHVEHRCNISWEI---SQASHYFHHLEF	167	
QY	157	ELQVNRGDPNVAVSPRRKLIISVDSRSVSLPLEFRKDSSEYELQVRAGMPGSSYQGTWSE	216	
Db	168	EARTLSPGHTWEEAP---LLTLKQKQEWICLETLPDQYEFQVRVKPLQGEF--TTWSP	222	
QY	217	WSDPVIPTQSEBELKEG---WNPHLLLLLLLVIPAFWSL-----KTHPLRLWLN-KKIW	268	
Db	223	WSQPLAFRTKPAALGKDTIPWLGHLVLGLSGAFGFIILVYLLINCNTGP-----WLKKYL	278	
QY	269	A--VPSPERFMPLYKGCSDGPKWVGAPFTGSSLELGFWSPEVPSTLEVSYCHPPRSPA	326	
Db	279	KNTPTDPSKFFQSLSSEHGGDVQKWLSSFFSSPFGGLAPEI-SPLEV-----L	328	



cytokine receptor common beta chain precursor - mouse

C:Species: Mus musculus (house mouse)  
C>Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 09-Jul-2004  
C:Accession: A35782

R:Gorman, D.M.; Itoh, N.; Kitamura, T.; Schreurs, J.; Yonehara, S.; Yahara, I.; Arai, K.  
Proc. Natl. Acad. Sci. U.S.A. 87, 5459-5463, 1990

A:Title: Cloning and expression of a gene encoding an interleukin 3 receptor-like protein  
A:Reference number: A35782; MUID:90319131; PMID:1695379

A:Accession: A35782

A:Molecule type: mRNA

A:Residues: 1-896 <OR>

A:Cross-references: UNIPROT:P26955; GB:M34397; NID:gl91821; PIDN:AAA37204.1; PID:9309101  
C:Comment: Mouse high-affinity IL-5, GM-CSF, and one class of high-affinity IL-3 receptor

C:Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor H  
C:Keywords: cytokine receptor; duplication; transmembrane protein

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-896/Product: cytokine receptor common beta chain #status predicted <MAT>

F:23-441/Domain: extracellular #status predicted <EXT>

F:29-235/Domain: cytokine receptor homology <CRS1>

F:253-434/Domain: cytokine receptor homology <CRS2>

F:442-463/Domain: transmembrane #status predicted <TM>

F:464-896/Domain: intracellular #status predicted <INT>

Query Match 7.9%; Score 233; DB 1: Length 896;

Best Local Similarity 20.4%; Pred. No. 1.3e-08;

Matches 113; Conservative 86; Mismatches 220; Indels 134; Gaps 23;

QY 22 DLVCTDYLQTVICILEMWN-----LHPSTLTLTWQDQYEELKDEATSCSLHRS 70

DB 250 NLQCFDGTQLSLHCSWEVWTTQTSVGLFYRPSVA-----PEEKCSFVVKEP 299

Q\* 71 ANNATHATYTCMDVHFHMAIDIFSVNITDQSGNYSQEGCSFLLA-ESIKPAPP-FNVTV 128

DB 300 PGASVYTRYHCSLPPEPSAHSQYTVSVK-----HLEQKFTMSYNHIQEPPTLNLT 353

QY 129 TFSQGNYSWRSYEDDPAPYMLKGLQYELQYRNRPDPAVSPRKLISVDSRSVLLPL 188

DB 354 N-RDYSLSHWETQKWAYSFI-----EHTFQVQYKKSQSDSWEDSKTENLDRAHMSDLS 404

QY 189 EPRKDSYSLQVRAQPMFGSSYQGTWSESDVIFQTSSEELKEGWNPHLLLLLVIVF 248

DB 405 QLEPDTSYCARVRKPI--SNYDGIWSKWESEYTKT-DWVPTLWVILVFLTLTLL 461

QY 249 IPAFSLKTHPLRWLKKWTWVSPERFPMPLYKCGSGDFKKVGAPFTGSSLELGPWSP 308

DB 462 ILRFQCVSYTRYRWKE--KIPNPSKSL-----FDGKGGLWP--- 499

QY 309 EYPSLEIVYSCHPP--RSPAKLQLTELQEPALVESDGVKPSFWPTAQNSGGSAYSEE 366

DB 500 --PGSMAAFATKPNPALQGPQSL-LAEQQ-----GESYAH 532

QY 367 RDRPYGLVSDIVTVL--DAEGPCTWPCSD--DCYPALDLDAGLEPSPGLDPLDAG 422

DB 533 EDNVSPLTIEDPIRPPSPGDTTPAASSESTQLPNVQEGTTPNRPKQLSFD-- 590

QY 423 TTVLSCGCVSAGSPGLGGP-----LGSLLDRKPLPADGE--DWAGGLPWGGRSPG-- 472

DB 591 -----FNGPYLGPQSHSLPDLPLQGLSPQVGGSLKPLPGSLEYMCLAPGQVQ 640

QY 473 -----VSEESAGSPLAGLMDTDFSGFVGDSCSPVECDFTSPGDEGPPRSYLQWV 525

DB 641 LVPLSQVMGQGMVDQCGSSLETSGSPVEKPNPPVELSMEEQEARNDP----- 691

QY 526 IPPPLSSPGPOAS 538

DB 692 VTLPISSGGPEGS 704

RESULT 5

A45268

interleukin-9 receptor precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 09-Jul-2004

C:Accession: A45268

R:Renauld, J.C.; Druet, C.; Kermouni, A.; Houssiau, F.; Uyttenhove, C.; Van Roost, E.;  
Proc. Natl. Acad. Sci. U.S.A. 89, 5690-5694, 1992

A:Title: Expression cloning of the murine and human interleukin 9 receptor cDNAs.

A:Reference number: A45268; MUID:92302307; PMID:1376929

A:Accession: A45268

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-468 <REN>

A:Cross-references: UNIPROT:Q01114; GB:M84746; NID:9194044; PIDN:AAA37871.1; PID:9194044

A>Note: authors translated the codon GGG for residue 394 as Glu

C:Keywords: glycoprotein; receptor; T-cell proliferation; transmembrane protein

Query Match 7.5%; Score 221.5; DB 2: Length 468;

Best Local Similarity 23.2%; Pred. No. 3.9e-08;

Matches 134; Conservative 60; Mismatches 181; Indels 203; Gaps 34;

QY 3 RGMAAPLLLLLLGGWG--CPDLVCTDYLQTVICILEMWNLHPSTLT-----TW---- 51

DB 36 RGVSVP-----EQGGGQKAGACTCLNSIYRIDC-----HWSAPELQGSRALWLLFT 83

QY 52 QDQYEELKDEAT-----SCSLHRSAHNA-----THATYTCMDVHFHMAIDIFSVNITDQSG 103

DB 84 SNQVTEIKHKCTFWDSMCTLVLPKEEVFLPFDNFITLHRCI---MGQE--QVSLVD--- 135

QY 104 NYSQEGSFLAESIKPAPPNV-TVTPSQGNYSWRSYEDDPAPYMLKGLQYELQYRN 162

DB 136 -----SOYLPRRHIKLDPSPDLSQNSVSSRCVLTWGINL---ALEPLITSLSYELAFKR 186

QY 163 RGDPAVSPRKLISVDSRSVLLPLEPRKDSYSELQVRA-----GPMPGSSYQGTW 214

DB 187 QEEAEWAHKKDRIQGV--TWLILEAVELNPGSIYEALRURVQMTLESYEDKTEGEYKSHW 244

QY 215 SEWSDPVTFQTSBELKEG-----WNPHLLLLLVIVFIPAFWSLK--THPLWRL-- 263

DB 245 SEWQPVSF--PSQRRQGLLVPRMWSASIL-----VVVPIFLTLTGFWHLLFKLSP 295

QY 264 -WKIWI--AVSPERFPMPLYKCGSGDFKKVGAPFTGSSLELGPWSPSTLEVYSCH 320

DB 296 RLKRIFYQNIPEAFPHLYSVYHGDQFSQWTGARRAG----- 333

QY 321 PPRSPAKLQLTELQEPALVESDGVKPSFWPTAQNSG---GSAYSERDRPYGLVSI- 376

DB 334 -----POARQNGVSTSSAGSES-----POARQNGVSTSSAGSES---SIW 353

QY 377 DTVTLDAEGPCTWPCSC-----EDDGYFALDLDAGLEPSPGLDPLDAGTTVLSCGCV 431

DB 354 EAVATLYSPACPVQFACLKWEATAPGPGI-----PGSEH-----VLPAGCL 396

QY 432 S-AGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSSEAGSPLAGLMDTDF 490

DB 397 ELEGQPSAYLP-----QEDWA---PLGSARP-PPPDSDSGS----- 428

QY 491 DSGFVGSDCSFVRCDFTS-PGDEGPPRSYLQWV 527

DB 429 -SDYCMILDCB--ECHLSAFPGHTESPELTTLAQPVALP 463

RESULT 6

A40091

interleukin-3 receptor beta chain precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 09-Jul-2004

C:Accession: A40091; A43022

R:Ito, N.; Yonehara, S.; Schreurs, J.; Gorman, D.M.; Maruyama, K.; Ishii, A.; Yahara, I.

Science 247, 324-327, 1990

A:Title: Cloning of an interleukin-3 receptor gene: a member of a distinct receptor gene

A:Reference number: A40091; MUID:90117145; PMID:2404337

A:Accession: A40091

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-878 <ITO>

A:Cross-references: UNIPROT:P26954





Best Local Similarity 22.0%; Pred. No. 1.4e-07;  
Matches 115; Conservative 61; Mismatches 179; Indels 167; Gaps 25;

Qy 15 QGNGCPCDLVCYTDYLQTVICILEMMNLHPTLTLTW-----QQQEELKDEAT-----SCS 66  
Db : : : : :  
Qy 44 EGGRKAGTFTCFNSVFRIDC---HWSA-FPGSRAMLLFTSNQGTDIKHKTFFWSRCT 99  
Db : : : : :  
Qy 67 LHRSAHNA-----THATTYCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAP 132  
Db LVLPLKEBAFLPFDFNTITLHRCV---MGQE--QVSLVD-----SOYLPRRHKLDP 145  
Qy 123 PFNV-TVTFSGOYNISWRSDYEDPAFYMLKGQLQVELQYENRGDPPAVSPRRKLISVDSR 181  
Db : : : : :  
Qy 146 PSDLQSNISSGRCVLTWGISF---GLEPLITSLSYELAFKRQBEAME-QARLKDRIVGVTT 201  
Qy 182 SVSLLPLEFRKRDSSYELOVRAA-----GPMFGSSYQGWTSEMSDVPVQTQSEELKEG 233  
Db WLVLEATELNPDITYEARLVQMALESYDDKDTEGEYYKSHSEWSQSVSPSPRRKTQG- 260  
Qy 234 WNPHLLLLLLL-----VVVFIPAFWSLK--THPLMRLWKKI-----WAVPSRRFFM 278  
Db : : : : :  
Qy 261 -----LLIPIRWQGSASILVAVIPILLTLGLIHFLRLSPVKGRIFYQNVPSPAFFF 312  
Qy 279 PLYKGCSDGFKKWGAFTGSSLSLELGWPSEVSTLEVSYCHPPSPAKELQLTELQEP 338  
Db : : : : :  
Qy 313 PLYSVYHGDFQTWIGARRAG-----PELDSDGSSDYCMCLDC 435  
Qy 339 ELVESDGVPKPSFWPTAQNSGGGAYSEERDRPYGLVSIDVTVLDAABGPCTWPCSCEDDG 398  
Db : : : : :  
Qy 333 -----PQARQDGA SAPGDSES-----SIWEAIATITYSPACSVQ- 367  
Qy 399 YPALDLLDAGLPGLGEDPLLDDAGTIVYLCGCYS-AGSPGLGGPLGSLDLRLKPPLADGE 457  
Db FPSLKWEA-----TAPGFPGP-PGSELVLPAGCLELEGQPSAYLP-----QE 408  
Qy 458 DWAGGLPWGSRSPCGVSESEAGSPLAGLDMDTFDSDGFVGSDC 499  
Db : : : : :  
Qy 409 DWA----PLGARP-----PELDSDGSSDYCMCLDC 435

RESULT 9  
ZUHR  
erythropoietin receptor precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 12-Feb-1993 #sequence revision 5-Apr-1995 #text change 09-Jul-2004  
C:Accession: A43799; A60160; A49824; A53958; A55280; I52563  
R:Jones, S.S.; D'Andrea, A.D.; Haines, L.L.; Wong, G.G.  
Blood 76, 31-35, 1990  
A>Title: Human erythropoietin receptor: cloning, expression, and biologic characterization  
A:Reference number: A43799; MUID:90304340; PMID:2163696  
A:Accession: A43799  
A:Molecule type: mRNA  
A:Residues: 1-508 <JUN>  
A:Cross-references: UNIPROT:P19235; GB:M60459; NID:g182244; PIDN:AAA52403.1; PID:g182245  
R:Winkelman, J.C.; Penny, L.A.; Deaven, L.I.; Forget, B.G.; Jenkins, R.B.  
Blood 76, 24-30, 1990  
A>Title: The gene for the human erythropoietin receptor: analysis of the coding sequence  
A:Reference number: A60160; MUID:90304334; PMID:2163695  
A:Accession: A60160  
A>Status: not compared with conceptual translation  
A:Molecule type: mRNA; DNA  
A:Residues: 1-101,'R',103-188,'RP',191-243,'E',245-508 <WIN>  
R:Noguchi, C.T.; Bae, K.S.; Chin, K.; Wada, Y.; Schechter, A.N.; Hankins, W.D.  
Blood 78, 2548-2556, 1991  
A>Title: Cloning of the human erythropoietin receptor gene.  
A:Reference number: A49824; MUID:92399733; PMID:1668606  
A:Accession: A49824  
A:Molecule type: DNA  
A:Residues: 1-508 <NOG>  
A:Cross-references: GB:545332; NID:g255496; PIDN:AAB23271.1; PID:g255497  
A:Experimental source: placenta  
A>Note: sequence extracted from NCBI backbone (NCBIN:113293, NCBIPI:113294)  
R:Ehrenman, K.; St. John, T.

Qy 375 SIDVTVLDAEGPCTWPCSCDDGYPALDDAGLEPSGLEDLLDAGTTVLSCGCVSAG 434  
Db 344 AVEPGT--DDEGPLLEPGVSEHAQTYLVLDKWLDR----- 378  
Qy 435 SPGLGGPLGSLIDRLKPLADGEDWAGLPGWGRSPGVGSEAGSPGLAGLMDMTDFSGF 494  
Db 379 -----NPSSED-----LP-----GPGG-----SVDIVAMDEGS 401  
Qy 495 VGSDCSPVECDFTSPGDEG-----PPRSYLQWVVP--PP 529  
Db 402 BASSCSALLA---SKPSPEGASAAFEYITILDPSQLLRPTWCPLEPP 447  
RESULT 10  
I56563  
C:Species: Rattus sp. (rat)  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-May-2004  
C:Accession: I56563  
R:Appel, K.; Buttini, M.; Sauter, A.; Gebicke-Haerter, P.J.  
J. Neurosci. 15, 5800-5809, 1995  
A:Title: Cloning of rat interleukin-3 receptor beta-subunit from cultured microglia and  
A:Reference number: I56563; MUID:95370942; PMID:7643220  
A:Accession: I56563  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-896 <RES>  
C:Cross-references: GB:S79263; NID:g1086954; PIDN:AAB35068.1; PID:g1086955  
C:Genetics:  
A:Gene: rIL-3Rbeta  
C:Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor h  
C:Keywords: cytokine receptor  
F:17-897/Domain: signal sequence #status predicted <SIG>  
F:253-433/Domain: cytokine receptor homology <CRS1>  
F:253-433/Domain: cytokine receptor homology <CRS2>  
Query Match 7.2%; Score 211.5; DB 2; Length 896;  
Best Local Similarity 21.7%; Pred. No. 4.5e-07;  
Matches 126; Conservative 79; Mismatches 228; Indels 147; Gaps 28;  
Qy 2 PRGMAAPLLLLLLOQWGCP-----DLVCYTYDLOTVICILEMWNHLPSTLTLTWQD 53  
Db 229 PSGWSPEV-----HWDSPTEDKARPQNLOCFDGIQSLNCSEWVWTKVTDVSFGLFY 281  
Qy 54 QYEELEKDEATCSLHRSNAHATHAYTCHMDVHFHMADDIFSVNITDQSGNYSECQSFL 113  
Db 282 SSSPXAGEKKCSPPVKELQASRYTRYHCSLNVSDPAHQSQTVSVK-----RUEQGRFI 335  
Qy 114 LA-ESIKPAPP-FNVTVTFSGOYNISWRSDYEDPAFYMLKGKLOQYELQYRNRPDPWAVSP 171  
Db 336 ESFNHIQWNPPTLNLTKN-RDSYSLHWETQKMSYFPI-----QHAFQVQYKKLDRWEDSK 390  
Qy 172 RKKLISVDSRSVLLPLEFRKDDSSYELQVRAGMPGSSYQGTWSEWSDPVIPTQOSEBLK 231  
Db 391 TENLNAHSMQD--LP-QLEPGCTSYCAKRVKTIK-EYKGLWSEWSECTWTTD----- 439  
Qy 232 EGW-NPHL--LLLLLVIVTIPA--FWSLKTPLRLWKKIWA VSPSEPFMPLYKGS 285  
Db 440 ---WNMPTLWILVFLITFLALRFGCIYGRKRKWKELIPNPSKSLJFQDQGGKL- 496  
Qy 286 GDFKXWVGAFTGSSLELGPWSPVFTLEVVSCHP-PRSPAKRLQLTELQPAELVSD 344  
Db 497 -----WPP--GSIVTFSSKNPTQGPQNLL-FSELQ----- 524  
Qy 345 GVPKPSFWPTAQNSGGSAYSEERDRPYGLVSDTVTL--DABGCTWPCSCDDGYPAL 402  
Db 525 -----GVSYTHLEDNEVSPLTIEDNIRDPSSGDPDTPAASSEP----- 564  
Qy 403 DLDAGLEPSGLE-DPLLDAGTTVLSCGCVSAGSPGLGGL-----GSLLD-----R 448  
Db 565 -----MEQSSNVQVDPPTLSGRPRKQLPSFDNGBYLGPPQSHSLPDLPGQLVSPQGVGS 619  
Qy 449 LKPLADGEDWAGLPGWGRSPGG-----VSESEAGSPLAGLMDMTDFSGFVGS 498

Db 620 LKPAL-----PGSLEYMCLPPGGQVQLVPLSQVMGQRDQVQCGSSLETSPSMESR 678  
Qy 499 CSSPVECDFTSPGDEGPRSYLRQWVVPPLSSSPGQAS 538  
Db 674 ESPPEVL-----KBEQEPRDN-----PVTLPFISSGGPKDS 704  
RESULT 11  
A39255  
cytokine receptor common beta chain precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 09-May-2004  
C:Accession: A39255  
R:Hayashida, K.; Kitamura, T.; Gorman, D.M.; Arai, K.; Yokota, T.; Miyajima, A.  
Proc. Natl. Acad. Sci. U.S.A. 87, 9655-9659, 1990  
A:Title: Molecular cloning of a second subunit of the receptor for human granulocyte-mac  
A:Reference number: A39255; MUID:91088571; PMID:1702217  
A:Accession: A39255  
A:Molecule type: mRNA  
A:Residues: 1-897 <HAY>  
C:Cross-references: GB:M38275  
C:Comment: The human high-affinity IL-3, IL-5, and GM-CSF receptors have ligand-specific  
C:Genetics:  
A:Gene: GDB:CSF2RB  
A:Cross-references: GDB:126838; OMIM:138981  
A:Map position: 22q13.1-22q13.1  
C:Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor h  
C:Keywords: alternative splicing; cytokine receptor; duplication; transmembrane protein  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:17-897/Domain: signal sequence #status predicted <EXT>  
F:17-443/Domain: extracellular #status predicted <CRS1>  
F:35-232/Domain: cytokine receptor homology <CRS2>  
F:250-431/Domain: cytokine receptor homology <CRS2>  
F:444-460/Domain: transmembrane #status predicted <TM>  
F:461-897/Domain: intracellular #status predicted <INT>  
Query Match 6.9%; Score 204; DB 1; Length 897;  
Best Local Similarity 22.6%; Pred. No. 1.5e-06;  
Matches 142; Conservative 66; Mismatches 219; Indels 200; Gaps 82;  
Qy 22 DLVCYTYDLOTVICILEMWNHLPSTLT--LTWQOYELKDEATSC-----SLHRSNAH- 72  
Db 247 NLECFDFAAVALSCSWEVKVASVSFGLFYKPSDPAGEECSFVLREGLSLTHRHC 306  
Qy 73 -----NATHATYTCMDVHFHMADDIFSVNITDQSGNYSECQSFLLAESIKKAPPNV 126  
Db 307 QIPVDPDATHGQY-----IVSV-----QPRRAEKHIKS-----SVNIQWAPP-SL 345  
Qy 127 TVTFSG-QYNISW-----RSDYEDPAFYMLKGKLOQYELQYRNRPDPWAVSPRRKLISVDS 180  
Db 346 NVTKDGSYSLRWETMKWRYEHIDTF-----ELQYRKDTATWKDSKTETL--QNA 394  
Qy 181 RSVLLPLEFRKDDSSYELQVRAGMPGSSYQGTWSEWSDPVIPTQOSEBLKEGNPHLLL 240  
Db 395 HSMALPALE--PSTRYWARVRV-RTSRTGYNGIWSSEARSBDTES--VLPMW----- 443  
Qy 241 LLLLIVIVTIPA-----FWSLKTPLRLWKKIWA VSPSEPFMPLYKGSQDFKWK-- 291  
Db 444 VLALIVPLTAVLALRFGCIYGRKRKWKELIPNPSKSLJFQ-----NGSALWPP 497  
Qy 292 --VGAPFTGSSLELGPWS---PEV-----PSTLE--VYSCHPPRSPAKRLQ 330  
Db 498 GSMAFTSGSPHQPGWGRSPFELEGVPFVGDSSEVSPLTIEDPKHVCDPSPGDDTTPA 57  
Qy 331 LTELQEPALVESDGVKPSFWPTAQNSGGSAYSEERDRPYGLVSDTVTLVLDABGCTW 390  
Db 558 ASDLPTEQPPSPGPPAASHTPEKQASS-----FDNFGPYLG 595  
Qy 391 P---CSCEDD-GYPALDLDAGLESP---GLEPDLDDAGTTVLSCGCVSAGSPGLG--- 439  
Db 596 PPHSRSLPDIILQGPPEPPQEGSGSQSPPGSLLEYLCLPAGGQVQLVPLQAQMGPGQAVEVE 555

QY 440 -----GPIGLSLDLRLKPPPLADGEDWAGGLPWGGRSP-----GGVSESEAGSPLAGLDM 487  
Db 656 RRPSSQAAGS-----PSLESG-----GGPAPPALGPVGGODQKDSVPALPMSG 700  
QY 488 DTDFSGFVGDCSSPVECDFT-----SPGDEGPP 516  
Db 701 DTEDPG-VASGVYSSADLVFTNSGASSVSLVPSLGLPSDQFPLCPLGLASGPPGAPGV 759  
QY 517 RSYLQWVVIPP-----PLSSQGP 535  
Db 760 KSGFEGYVELPPIEGRSRPNRPVP 786

RESULT 12  
A32385  
erythropoietin receptor precursor, membrane-bound form - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 28-Sep-1990 #sequence revision 05-Apr-1995 #text\_change 09-Jul-2004  
C:Accession: A41686; J13249  
R:Hino, M.; Tojo, A.; Misawa, Y.; Morii, H.; Takaku, F.; Shibuya, M.  
Mol. Cell. Biol. 11, 5527-5533, 1991  
A:Title: Unregulated expression of the erythropoietin receptor gene caused by insertion  
A:Reference number: A41686; MUID:92017832; PMID:1656233  
A:Accession: A41686  
A:Molecule type: mRNA  
A:Residues: 1-507 <HIN>  
A:Cross-references: UNIPROT:P14753; GB:S59388; NID:G237036; PIDN:AAB20029.1; PID:G237037  
A:Experimental source: murine erythroleukemia (MEL) cell line F5-5  
R:D'Andrea, A.D.; Lodish, H.F.; Wong, G.G.  
Cell 57, 277-285, 1989  
A:Title: Expression cloning of the murine erythropoietin receptor.  
A:Reference number: A32385; MUID:89195238; PMID:2539263  
A:Accession: A32385  
A:Molecule type: mRNA  
A:Residues: 1-507 <DAA>  
A:Cross-references: J04843; NID:G193090; PIDN:AAA17571.1; PID:G309219  
A:Experimental source: murine erythroleukemia (MEL) cells, subclone 745  
R:Kuramochi, S.; Ikawa, Y.; Todokoro, K.  
J. Mol. Biol. 216, 567-575, 1990  
A:Title: Characterization of murine erythropoietin receptor genes.  
A:Reference number: S13249; MUID:91080149; PMID:2175360  
A:Accession: S13249  
A:Molecule type: DNA; mRNA  
A:Residues: 1-507 <URS>  
A:Cross-references: EMBL:X53081; NID:G50861; PIDN:CAA37248.1; PID:G50862  
A:Experimental source: murine erythroleukemia K-1 cells  
C:Genetics:  
A:Introns: 39/1; 83/2; 142/1; 194/3; 246/1; 275/2; 304/3  
C:Superfamily: erythropoietin receptor; cytokine receptor homology  
C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-507/Product: erythropoietin receptor #status predicted <MAT>  
F:25-249/Domain: extracellular #status predicted <EXT>  
F:52-238/Domain: cytokine receptor homology <CRS>  
F:250-271/Domain: transmembrane #status predicted <TMM>  
F:272-507/Domain: intracellular #status predicted <INT>  
F:52-62, 90-106/Disulfide bonds: #status predicted  
F:75/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.8%; Score 201; DB 1; Length 507;  
Best Local Similarity 23.1%; Pred. No. 1.2e-06;  
Matches 117; Conservative 60; Mismatches 188; Indels 142; Gaps 27;

QY 2 PRGWAAPLILLLLQGGW-----GCPDLVCYTDVLTQVICILEMW 40  
Db 10 PR--VGPICLLLAGAWAPSLPDPKESKAALLASRGSELLCTQRLDVLVCFWE-- 65  
QY 41 NLHPSTLTWTQDQVEELKDEATSCSLHRSAAHNAHTATYTCM----DVHFHMADDFSVN 97  
Db 66 EAASGMDFNYFSYQLEGESKSCSLHQAPTVRGSVRFWCSLPTADTSSFPV---LELQ 122  
QY 98 ITDQGN--YSQ-----ECGSFLLAES-----IKPAPPFNVTTFSCQYNIS 137

Db 123 VTEASGSPRYHRIIHIINEVLLDAPAGLLARRAEBGSHVLRWLWLPPLPGAPMTTHIRYEV- 181  
QY 138 WRSDYEDPAFYMLKGKQYELQYRNRPDPWAPRPRKLISVDSRSVSLPLPLEFRKDSYVE 197  
Db 182 -----DVSAGNR-----AGGTQREVLEGRTECVLS-NLRGGTRYT 216  
QY 198 LQVRAGPMPGSSYQCTWSESDPVIFQTSSELKSGWNPPLHLLLLLVIVFIP---AFWS 254  
Db 217 FAVRA-RMAEPSFGFSWSEPAALLTASD-----LDP-LILTLSLILVLISLLLTUVA 269  
QY 255 LKTHPLWRLWKIIV-APVSPRFRFMPLYKGGSGDFKKW---GAPFTGSSLELGPWSPE 309  
Db 270 LLSSHER-TLQKIWPPIPSESEFGLFTTHKGNFQLMLQORDGCLW-----WSPG 319  
QY 310 VPSTLEVYSHPPRSPAKRLQITELQEPALVESGVP-----KPSFWPTAONGSGSAY- 363  
Db 320 -----SSPDEPPA---HLEVLSEPRWAVTQAGDPGADDEGPLLEPVGSEHAQDTYL 368  
QY 364 -----SEERDRPYGLVSTDTVTVDLDAEGPCTWPCSCEDDGYPALDLDAGLEPS 411  
Db 369 VLDKMLLPRTPCSENLSPGG--SVDPTMDSEATSSCPSDLASKPRP-----EGTSFS 421  
QY 412 PGLEDPLLDAGTTVLSCCVCVSAGSPGL 438  
Db 422 -SFEVTILDPSQLL---CPRALPPEL 444

RESULT 13  
A46713  
erythropoietin receptor precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
R:Masuda, S.; Nagao, M.; Takahata, K.; Konishi, Y.; Gallyas Jr., F.; Tabira, T.; Sasaki, J. Biol. Chem. 268, 11208-11216, 1993  
A:Title: Functional erythropoietin receptor of the cells with neural characteristics. C  
A:Reference number: A46713; MUID:93266574; PMID:7684373  
A:Accession: A46713  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-507 <MAS>  
A:Cross-references: UNIPROT:Q07303; GB:D13566; NID:G286209; PIDN:BAA02761.1; PID:G286210  
A:Experimental source: PC12 and erythroid cells  
A:Note: sequence extracted from NCBI backbone (NCBIN:132811, NCBIP:132813)  
C:Superfamily: erythropoietin receptor; cytokine receptor homology  
C:Keywords: cytokine receptor; glycoprotein; transmembrane protein  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-507/Product: erythropoietin receptor #status predicted <MAT>  
F:25-249/Domain: extracellular #status predicted <EXT>  
F:52-238/Domain: cytokine receptor homology <CRS>  
F:250-271/Domain: transmembrane #status predicted <TMM>  
F:272-507/Domain: intracellular #status predicted <INT>  
F:75/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.6%; Score 195; DB 1; Length 507;  
Best Local Similarity 21.4%; Pred. No. 3.2e-06;  
Matches 126; Conservative 70; Mismatches 194; Indels 198; Gaps 32;

QY 2 PRGWAAPLILLLLQGGW-----GCPDLVCYTDVLTQVICILEMW 40  
Db 10 PR--VSPICLLLAGAWASSPSLDPKESKAALLASRGSELLCTQRLDVLVCFWE-- 65  
QY 41 NLHPSTLTWTQDQVEELKDEATSCSLHRSAAHNAHTATYTCM----DVHFHMADDFSVN 97  
Db 66 EAASGMDFNYFSYQLEGESKSCSLHQAPTVRGSMRFWCSLPTADTSSFPV---LELQ 122  
QY 98 ITDQGN--YSQ-----ECGSFLLAES-----IKPAPPFNVTTFSCQYNIS 137  
Db 123 VTEASGSPRYHRIIHIINEVLLDAPAGLLARRAEBGSHVLRWLWLPPLPGAPMTTHIRYEV- 181  
QY 138 WRSDYEDPAFYMLKGKQYELQYRNRPDPWAPRPRKLISVDSRSVSLPLPLEFRKDSYVE 197  
Db 182 -----DVSAGNR-----AGGTQREVLEGRTECVLS-NLRGGTRYT 216



acellular domain and may encode a soluble form of the receptor  
R:Harada, N.; Castile, B.E.; Gorman, D.M.; Itoh, N.; Schreurs, J.; Barrett, R.L.; Howard,  
Proc. Natl. Acad. Sci. U.S.A. 87, 857-861, 1990  
A:Title: Expression cloning of a cDNA encoding the murine interleukin 4 receptor based o  
A:Reference number: A34861; MUID:90138976; PMID:2405398  
A:Accession: A34861  
A:Molecule type: mRNA  
A:Residues: 1-810 <HAR>  
A:Cross-references: GB:M29854; NID:gl98346; PIDN:AAA39297.1; PID:g309407  
R:Wrighton, N.C.; Campbell, L.A.; Lee, F.D.  
Growth Factors 6, 103-118, 1992  
A:Title: The murine interleukin-4 receptor gene: Genomic structure, expression and poten  
A:Reference number: I54232; MUID:92265335; PMID:1534014  
A:Accession: I54232  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-73, '1', '75-333', 'P', '335-810' <RES>  
A:Cross-references: GB:M64879; NID:gl98359; PIDN:AAB59727.1; PID:g198361  
C:Genetics:  
A:Introns: 24/1; 71/2; 122/1; 172/3; 225/1; 258/2; 284/3; 301/2  
C:Superfamily: interleukin-4 receptor; cytokine receptor homology  
C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein  
F:1-25/Domain: signal sequence #status predicted <SIG>  
F:26-810/Product: interleukin-4 receptor #status experimental <MAT>  
F:26-233/Domain: extracellular #status predicted <EXT>  
F:34-219/Domain: cytokine receptor homology <CRS>  
F:234-257/Domain: transmembrane #status predicted <TM>  
F:258-810/Domain: intracellular #status predicted <INT>  
F:72,129,135,163,177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.4%; Score 189.5; DB 1; Length 810;  
-Best Local Similarity 20.9%; Pred. No. 1.4e-05;  
Matches 159; Conservative 70; Mismatches 222; Indels 309; Gaps 42;  
QY 9 LLLLLLQGGCGPDL---VCYTDYLQTVICILEMNLH-----PSTLTITMODOVEELKD 60  
DB 15 LLLLLVTGSGSKVLGEPTCFSDYIRTSCTC---EWFDSAVDCSSQCLHYELMFEFSE 71  
QY 61 EATSCSLHRSAINATHATYTCMVPHFMADDIFSVNIITDQSGNYSQEC-----GS 111  
DB 72 NLTCI-----PRNSASTVCVCHE-----MNRPVQSDRYQMELWAEHRQLWQGS 115  
QY 112 FLAASIKPAPFNTV---TFSGQYNIWSRDY-----EDPAFYML 150  
DB 116 FSPGNVKEPLADNLTHTNVSDLEMLLTWNLYPNLNLLYKDLISMVNIREDNPAEFTV 175  
QY 151 KGLQVELQYNRGDPWVSPRRKLTISVDSRSVLLPLEFRKDSYVELQVRAGMPGSSY 210  
DB 176 -----YNYTK---EPRLSFPINILMS-----GVYTYARV---VRSQIL 209  
QY 211 QCTWSESDPVITFQOSEBELKEGNPHLLLLL-----LVIVFIPAFWSLKTHTPLWR 262  
DB 210 TGTWSEWSPSIT-----WYNHFQPLIQLRPLGVTISCLCIPLCFCYFSITK 258  
QY 263 LKKKIW--AVSPERFFM-----PLYKGC----- 284  
DB 259 I-KKIWDQIPTAPSPVAIIIQDAQVPLMDKQTSQESTKYPHMKTKLDKLLPCLLKH 317  
QY 285 ----SGDFKKWGPFTGSSLELGP--WSP-EVPSTLEVYSCHPPSPAKRLQLTELOE- 336  
DB 318 RVKKTDFPK--AAP-TKSLQSPGKAGCMEVSRIV-----LWPNVSVSVVRCMELFEA 370  
QY 337 PAELV--ESDGVKPSFWNTAQNSGGSAYSE--ERDRPYGLVSIIDTVTVLDAE----- 385  
DB 371 PVQNVEEDEIVKEDLSMSPNSGCGFQESQADIMARLTENLFSDLLEAENGGLGQSA 430  
QY 386 -----GECTWPC-----SCDDGYPALDLDAGLEFSPGLEDPILLDAG 422  
DB 431 LAESCSPLPSGSGQASVSWACLPMGPSEATCQVTEQPS-----HFGPLSGSPAQAP 483  
QY 423 TTVLSCG-----CVSAGSPGLGGLSLDLRLK----- 450  
DB 484 T--LACTQVPLVADNPATYRFSDCSPAPNPEGLAPSQQQADHLEEEEPSPADPHSSG 541

Search completed: July 9, 2005, 11:47:52  
Job time : 46 secs

QY 451 PPLADGEDW-----AGG--LPWGG-----RSPGGVSESEAGSP 481  
DB 542 PPMQPVESWEQILHMSVLQHGAAGSTPAPAGGYQEFVQAVKQGAQDEGVGVRPSGDP 601  
QY 482 -----LAGLMDMT-----FDSGFVG-----SDCSSPVECDFT----- 508  
DB 602 GYKAFSSLLSSNGIRGDTAAAGTDDHGCGYKFPQNPVNPQSPSSVPL-----FTFGLDTELS 658  
QY 509 -SPGDEGPPRSYLR-----QWVVIPLPLSS--POP 535  
DB 659 PSPLNSDPKSPPECGLGLELGLKGGDWKARPPADQVPKP 698

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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: July 9, 2005, 11:28:19 ; Search time 161 Seconds  
(without alignments)  
1292.404 Million cell updates/sec

Title: US-10-620-169-4  
Perfect score: 2958  
Sequence: 1 MPRGWAEPLLLLLGQWGC.....YLRQWVIPPPLSSPGPOAS 538

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2958	100.0	538	2 AAY27450	Human MU-
2	2958	100.0	538	3 AAB18634	A human z
3	2958	100.0	538	3 AAY45031	HUMAN Orp
4	2958	100.0	538	3 AAY69886	Human hae
5	2958	100.0	538	3 AAY79312	Human cyt
6	2958	100.0	538	4 AAB48001	Human IL-
7	2958	100.0	538	5 ABB81960	Human 164
8	2958	100.0	538	5 AAU11912	Human MU-
9	2958	100.0	538	5 AAE13726	Human sol
10	2958	100.0	538	5 AAU11978	Human zai
11	2958	100.0	538	6 ABR61402	Human IL-
12	2958	100.0	538	7 AAE14939	Human int
13	2958	100.0	538	7 ABE62888	Human MU-
14	2958	100.0	538	7 ABW00881	Human cyt
15	2958	100.0	538	7 ADG87460	Human zai
16	2958	100.0	538	7 ADH44685	Human zai
17	2958	100.0	538	7 ADI10121	Human int
18	2958	100.0	538	8 ADH10505	Human int
19	2958	100.0	538	8 ADJ25623	Human int
20	2958	100.0	538	8 ADM83456	Human PRO
21	2958	100.0	538	8 ADI91861	Human zai
22	2958	100.0	538	8 ADP19844	Human zai
23	2958	100.0	538	8 ADS82585	Interleuk
24	2951	99.8	538	3 AAY94304	Human HNO
25	2951	99.8	538	4 AAU08728	Human HNO

26	2933	99.2	538	4 AAE02459	Human DNA
27	2905	98.2	538	3 AAY69888	Mouse hae
28	2817	95.2	568	3 AAY94305	Human HNO
29	2817	95.2	568	4 AAE02457	Human DNA
30	2817	95.2	568	4 AAU08729	Human HNO
31	2817	95.2	568	5 AAE13738	Human sol
32	1899.5	64.2	361	3 AAY69883	Human hae
33	1735.5	58.7	529	3 AAY79320	Mouse cyt
34	1735.5	58.7	529	5 AAU11915	Mouse MU-
35	1735.5	58.7	529	5 AAE13730	Mouse sol
36	1735.5	58.7	529	6 ABR61405	Murine IL
37	1735.5	58.7	529	7 ABU62891	Mouse MU-
38	1735.5	58.7	529	7 ABW00888	Mouse zai
39	1735.5	58.7	529	7 ADG87543	Mouse zai
40	1735.5	58.7	529	8 ADM83539	Mouse zai
41	1735.5	58.7	529	8 ADS82587	Interleuk
42	1729.5	58.5	529	4 AAB48002	Murine IL
43	1729.5	58.5	529	5 ABB81961	Mouse 164
44	1729.5	58.5	529	5 ABE24986	Mouse OCR
45	1729.5	58.5	529	5 ABB33048	Mouse OCR

## ALIGNMENTS

RESULT 1  
AAY27450  
ID AAY27450 standard; protein; 538 AA.  
XX  
AC AAY27450;  
XX  
DT 26-NOV-1999 (first entry)  
XX  
DE Human MU-1 hematopoietin receptor protein.  
XX  
KW MU-1 hematopoietin receptor protein; e MU-1 protein; gene therapy;  
KW cell proliferation; cytokine production; immune response; cancer;  
KW autoimmune disease; transplant rejection; hematopoiesis; anemia;  
KW gene mapping; nutritional supplement; human.  
XX  
OS Homo sapiens.  
XX  
PN WO9947675-A1.  
XX  
PD 23-SEP-1999.  
XX  
PF 17-MAR-1999; 99WO-US005854.  
XX  
PR 17-MAR-1999; 98US-00040005.  
XX  
PA (GENY ) GENETICS INST INC.  
XX  
PI Donaldson D, Ungar M;  
XX  
DR WPI; 1999-562115/47.  
XX  
DR N-PSDB; AA207535.  
XX  
PT New nucleic acid encoding the MU-1 hematopoietin receptor protein, used  
PT for treating e.g. cancer, autoimmune disease or abnormal hematopoiesis.  
XX  
PS Claim 9; Page 33-35; 37pp; English.  
XX  
CC This represents a MU-1 hematopoietin receptor protein. The protein can be  
CC produced by standard recombinant methodology. The MU-1 protein has the  
CC biological activity of the MU-1 hematopoietin receptor superfamily chain.  
CC It is used to screen for specific binding agents; to raise specific  
CC antibodies; as assay reagents, tissue markers etc. and therapeutically  
CC (optionally expressed from the MU-1 gene by gene therapy). Many possible  
CC activities/uses of the MU-1 protein are described without supporting  
CC evidence, e.g. they regulate cell proliferation and differentiation,  
CC induce production of cytokines, stimulate or suppress an immune response  
CC (e.g. for treating immune deficiency of any etiology, cancer or  
CC autoimmune disease, and for preventing transplant rejection) and regulate

CC of hematopoiesis, e.g. for treating anemia. The MU-1 gene is used as a  
CC research reagent, for recombinant production of the protein, as tissue or  
CC molecular weight marker, for gene mapping; for production of anti-DNA or  
CC anti-protein antibodies etc. the MU-1 protein and the nucleic acids are  
CC also useful as nutritional supplements or sources and the antibodies can  
CC be used therapeutically, as assay reagents and for affinity purification  
XX  
XX  
SQ Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 2; Length 538;  
Best Local Similarity 100.0%; Pred. No. 6.2e-240;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MPRGWAAPLLLLLLQGGGCPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOVEELKD 60  
DB 1 MPRGWAAPLLLLLLQGGGCPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOVEELKD 60  
QY 61 EATCSLHRSAHNATHATYTTCHMDVHFHMADDIFSVNITDQSGNYSCQSGFLLAESIKP 120  
DB 61 EATCSLHRSAHNATHATYTTCHMDVHFHMADDIFSVNITDQSGNYSCQSGFLLAESIKP 120  
QY 121 APPFNVTTFSGQYNIWSRSDYEDPAFYLKGLQYELQYRNRPWAVSPRKLISYDS 180  
DB 121 APPFNVTTFSGQYNIWSRSDYEDPAFYLKGLQYELQYRNRPWAVSPRKLISYDS 180  
QY 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLLL 240  
DB 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLLL 240  
QY 241 LLLLVIVIFAPFWSLTKTHPLWRLWKIWAIVSPERFFMPLYKGCSDGPKKVGWGAFTGSS 300  
DB 241 LLLLVIVIFAPFWSLTKTHPLWRLWKIWAIVSPERFFMPLYKGCSDGPKKVGWGAFTGSS 300  
QY 301 LELGWPSEVPSTLEVYSCHPSPAPKQLQTLTEQPAELVESDGVKPSFWPTAQNCGG 360  
DB 301 LELGWPSEVPSTLEVYSCHPSPAPKQLQTLTEQPAELVESDGVKPSFWPTAQNCGG 360  
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLD 420  
DB 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLD 420  
QY 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
DB 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
QY 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLQWVVIPIPLSSPGQAS 538  
DB 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLQWVVIPIPLSSPGQAS 538

## RESULT 2

AAB18634  
ID AAB18634 standard; protein; 538 AA.

XX  
AC AAB18634;

XX  
DT 22-JAN-2001 (first entry)

XX  
DE A human zalphall ligand polypeptide.

XX  
KW zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;  
KW tumorigenesis; leukaemia; hematopoiesis; B cell tumour.

XX  
OS Homo sapiens.

XX  
PN WO200053761-A2.

XX  
PD 14-SEP-2000.

XX  
PF 09-MAR-2000; 2000WO-US006067.

XX  
PR 09-MAR-1999; 99US-00264908.

PR 11-MAR-1999; 99US-00265992.

PR 01-JUL-1999; 99US-0142013P.

XX (ZYMO ) ZYMOGENETICS INC.

XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;

PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;

XX WPI; 2000-565600/52.

XX N-PSDB; AAA75557.

XX New human cytokine, designated zalphall ligand, useful for stimulating

PT the proliferation and/or development of hematopoietic cells in vitro and

PT in vivo, and for treating tumorigenesis.

XX Disclosure; Page 255-256; 256pp; English.

XX The present sequence represents a human zalphall ligand polypeptide,  
CC which is a cytokine. The zalphall ligand is useful for stimulating the  
CC proliferation and development of haematopoietic cells in vitro and in  
CC vivo. Zalphall ligand polynucleotides can be used as primers or probes  
CC for cloning the zalphall gene. The zalphall ligand is useful for treating  
CC tumorigenesis. A zalphall ligand-saporin fusion toxin may be used for  
CC treating leukaemias and lymphomas. Antagonists against zalphall ligand  
CC are useful as research reagents for characterizing ligand-receptor  
CC interaction. Antagonists are also useful for inhibiting expansion,  
CC proliferation, activation and differentiation of cells involved in  
CC regulating hematopoiesis. The zalphall ligand may also be used to  
CC stimulate an immune response against B cell tumour, a virus, a parasite  
CC or a bacterium. The zalphall polypeptides, polynucleotides, antagonists,  
CC agonists and antibodies are also useful for the detection, diagnosis,  
CC prevention, and treatment of diseases associated with a zalphall ligand  
CC genetic defect

XX SQ Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 3; Length 538;  
Best Local Similarity 100.0%; Pred. No. 6.2e-240;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGWAAPLLLLLLQGGGCPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOVEELKD 60  
DB 1 MPRGWAAPLLLLLLQGGGCPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOVEELKD 60  
QY 61 EATCSLHRSAHNATHATYTTCHMDVHFHMADDIFSVNITDQSGNYSCQSGFLLAESIKP 120  
DB 61 EATCSLHRSAHNATHATYTTCHMDVHFHMADDIFSVNITDQSGNYSCQSGFLLAESIKP 120  
QY 121 APPFNVTTFSGQYNIWSRSDYEDPAFYLKGLQYELQYRNRPWAVSPRKLISYDS 180  
DB 121 APPFNVTTFSGQYNIWSRSDYEDPAFYLKGLQYELQYRNRPWAVSPRKLISYDS 180  
QY 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLLL 240  
DB 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLLL 240  
QY 241 LLLLVIVIFAPFWSLTKTHPLWRLWKIWAIVSPERFFMPLYKGCSDGPKKVGWGAFTGSS 300  
DB 241 LLLLVIVIFAPFWSLTKTHPLWRLWKIWAIVSPERFFMPLYKGCSDGPKKVGWGAFTGSS 300  
QY 301 LELGWPSEVPSTLEVYSCHPSPAPKQLQTLTEQPAELVESDGVKPSFWPTAQNCGG 360  
DB 301 LELGWPSEVPSTLEVYSCHPSPAPKQLQTLTEQPAELVESDGVKPSFWPTAQNCGG 360  
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLD 420  
DB 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLD 420  
QY 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
DB 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
QY 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLQWVVIPIPLSSPGQAS 538

```

Db      481 PLAGLDMDTFDSGFVSCDCSSPVECDFTSPGDEGPRSYLRQWVIPPPLSSPGPOAS 538
RESULT 3
AAV45031
ID      AAY45031 standard; protein; 538 AA.
AC      AAY45031;
XX
XX
DT      31-MAY-2000 (first entry)
DE      HUMAN Orphan Cytokine Receptor 10 (OCR10)-A polypeptide.
KW      Human; Orphan Cytokine Receptor 10-A; OCR10-A; cytokine; screen;
KW      cognate ligand; treatment; endocrine disorder; immune disorder.
XX
XX      Homo sapiens.
XX      WO200008152-A1.
XX      17-FEB-2000.
XX
XX      16-JUL-1999; 99WO-US016060.
XX
XX      04-AUG-1998; 98US-00128820.
XX
XX      (REGG-) REGENERON PHARM INC.
XX
XX      Masiakowski PJ, Morris J, Valenzuela DM;
XX      WPI: 2000-205707/18.
XX      N-PSDB; AA250748.
XX
XX      New HUMAN orphan cytokine receptors 10 and 10-A useful for screening for
XX      drugs e.g. receptor agonists that may mediate survival and
XX      differentiation in cells naturally expressing the receptor and for
XX      screening for cognate ligands.
XX
XX      Example 10; Page 39-41; 54pp; English.
XX
XX      The present sequence is that of HUMAN Orphan Cytokine Receptor 10-A
XX      (OCR10-A) polypeptide. It is expressed at high levels in spleen, thymus,
XX      peripheral blood leucocytes and lymph nodes and moderately in heart and
XX      placenta. It has a role in immune system and cytokine function. It is
XX      useful in screening for cognate ligands or drugs that mediate survival
XX      and differentiation of cells expressing this receptor. Modified HUMAN
XX      OCR10-A or its agonist can be used in the treatment of endocrine or
XX      immune disorders
XX
XX      Query Match      100.0%; Score 2958; DB 3; Length 538;
XX      Best Local Similarity 100.0%; Pred. No. 6.2e-240;
XX      Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      1 MPRGWAAPLLLLLGGGWCPCDLYCYTDYLTQVTCILEMNLHPSTLTLTWQDQVEELKD 60
Db      1 MPRGWAAPLLLLLGGGWCPCDLYCYTDYLTQVTCILEMNLHPSTLTLTWQDQVEELKD 60
QY      61 EATCSLHSAHNATHATYTCMDVHFHFWADDIFSVNITDQSGNYSQECGSFLAESIKP 120
Db      61 EATCSLHSAHNATHATYTCMDVHFHFWADDIFSVNITDQSGNYSQECGSFLAESIKP 120
QY      121 APPFNVTTFSGOYNISWRSYEDDPAFYMLKGLQYELQYRNKRGDPWAVSPRKLISVDS 180
Db      121 APPFNVTTFSGOYNISWRSYEDDPAFYMLKGLQYELQYRNKRGDPWAVSPRKLISVDS 180
QY      181 RSVLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLL 240
Db      181 RSVLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLL 240
QY      241 LLLLIVVIFPAPWSLKTHPLWKLKINAVPSPERFFMPLYKGCSDGFKKWWGAPFTGSS 300

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Db      241 LLLLIVVIFPAPWSLKTHPLWKLKINAVPSPERFFMPLYKGCSDGFKKWWGAPFTGSS 300
QY      301 LELGPMSPVPSTLEVYSCHPPRSPAKRLQLTELQSPAEELVESDGVKPKSFMPTAQNSGG 360
Db      301 LELGPMSPVPSTLEVYSCHPPRSPAKRLQLTELQSPAEELVESDGVKPKSFMPTAQNSGG 360
QY      361 SAYSEERDRPYGLVSDITVTVDAGPCTWPCSCDDGYPALDLDAGLESPGLEDPLLD 420
Db      361 SAYSEERDRPYGLVSDITVTVDAGPCTWPCSCDDGYPALDLDAGLESPGLEDPLLD 420
QY      421 AGTTVLSCGCVSAGSPGLGGLGSLDLRLKPLADGEDWAGLPMGGRSPGGVSESEAGS 480
Db      421 AGTTVLSCGCVSAGSPGLGGLGSLDLRLKPLADGEDWAGLPMGGRSPGGVSESEAGS 480
QY      481 PLAGLDMDTFDSGFVSCDCSSPVECDFTSPGDEGPRSYLRQWVIPPPLSSPGPOAS 538
Db      481 PLAGLDMDTFDSGFVSCDCSSPVECDFTSPGDEGPRSYLRQWVIPPPLSSPGPOAS 538
RESULT 4
AAV69886
ID      AAY69886 standard; protein; 538 AA.
XX
XX      AC      AAY69886;
XX
XX      DT      24-MAY-2000 (first entry)
XX
XX      DE      Human haemopoietin receptor family member NR8gamma.
XX
XX      KW      Haemopoietin receptor family; NR8; antibody; diagnosis;
XX      blood formation disorder.
XX
XX      OS      Homo sapiens.
XX
XX      PN      WO9567290-A1.
XX
XX      PD      29-DEC-1999.
XX
XX      PF      23-JUN-1999; 99WO-JP003351.
XX
XX      PR      24-JUN-1998; 98JP-00214720.
XX      19-OCT-1998; 98JP-00297409.
XX
XX      PA      (CHUS ) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
XX      PI      Nomura H, Maeda M;
XX
XX      DR      WPI: 2000-116933/10.
XX      N-PSDB; AA259240.
XX
XX      Hemopoietin receptor protein family NR8 used for diagnosis of blood
XX      formation disorders.
XX
XX      PS      Claim 4; Fig 9-10; 176pp; Japanese.
XX
XX      CC      This sequence represents a novel haemopoietin receptor protein family
XX      NR8, designated NR8gamma. Antibodies to the NR8 family proteins are used
XX      for the diagnosis of blood formation disorders. Compounds identified as
XX      binding to the proteins are used for the treatment of such disorders
XX
XX      SQ      Sequence 538 AA;
XX
XX      Query Match      100.0%; Score 2958; DB 3; Length 538;
XX      Best Local Similarity 100.0%; Pred. No. 6.2e-240;
XX      Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      1 MPRGWAAPLLLLLGGGWCPCDLYCYTDYLTQVTCILEMNLHPSTLTLTWQDQVEELKD 60
Db      1 MPRGWAAPLLLLLGGGWCPCDLYCYTDYLTQVTCILEMNLHPSTLTLTWQDQVEELKD 60
QY      61 EATCSLHSAHNATHATYTCMDVHFHFWADDIFSVNITDQSGNYSQECGSFLAESIKP 120
Db      61 EATCSLHSAHNATHATYTCMDVHFHFWADDIFSVNITDQSGNYSQECGSFLAESIKP 120
QY      121 APPFNVTTFSGOYNISWRSYEDDPAFYMLKGLQYELQYRNKRGDPWAVSPRKLISVDS 180
Db      121 APPFNVTTFSGOYNISWRSYEDDPAFYMLKGLQYELQYRNKRGDPWAVSPRKLISVDS 180
QY      181 RSVLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLL 240
Db      181 RSVLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLL 240
QY      241 LLLLIVVIFPAPWSLKTHPLWKLKINAVPSPERFFMPLYKGCSDGFKKWWGAPFTGSS 300

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QY 121 APPENVVTFSGQYNISWRSDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRRKLIISYDS 180  
DB 121 APPENVVTFSGQYNISWRSDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRRKLIISYDS 180  
QY 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEELKEGWNPHLLL 240  
DB 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEELKEGWNPHLLL 240  
QY 241 LLLLIVVTFPAFWSLKTPLMLKWKIWAQVSPERFPMPLKYGCGSDGPKKVGAPFTGSS 300  
DB 241 LLLLIVVTFPAFWSLKTPLMLKWKIWAQVSPERFPMPLKYGCGSDGPKKVGAPFTGSS 300  
QY 301 LELGWPSEVPSTLEVYSCHPSPRPAKRLQELQEPALVESDCGVPKPSFWPTAQNSSG 360  
DB 301 LELGWPSEVPSTLEVYSCHPSPRPAKRLQELQEPALVESDCGVPKPSFWPTAQNSSG 360  
QY 361 SAYSEERDRPYGLVSDITVTLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLEDDPLD 420  
DB 361 SAYSEERDRPYGLVSDITVTLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLEDDPLD 420  
QY 421 ACTTVLSCCVCVAGSPGLGPGISLLDLKPLPADGEDWAGGLPWGGRSPGVSESEAGS 480  
DB 421 ACTTVLSCCVCVAGSPGLGPGISLLDLKPLPADGEDWAGGLPWGGRSPGVSESEAGS 480  
QY 481 PLAGLDMOTFDSGFGVSCSSPVECDFTSPGDEGPPRSYLRQWVVIPLPSRGPQAS 538  
DB 481 PLAGLDMOTFDSGFGVSCSSPVECDFTSPGDEGPPRSYLRQWVVIPLPSRGPQAS 538  
RESULT 5  
AY979312  
AY979312 standard; protein; 538 AA.  
AY979312;  
18-JUL-2000 (first entry)  
Human cytokine receptor zalphall.  
Cytokine receptor; zalphall; human; chromosome 16p11.1; apoptosis;  
signal transduction; growth factor; cancer; tumour; infection;  
immunosuppressive; immunostimulant; autoimmune disease; leukaemia;  
lymphoma; transplant rejection; therapy; diagnosis.  
Homo sapiens.  
Key Location/Qualifiers  
FT 1..19 /note= "signal peptide"  
FT 20..538 /note= "mature protein; a polypeptide comprising the mature protein is specifically claimed in Claim 27(d)"  
FT 20..237 /note= "cytokine-binding domain; a polypeptide comprising this domain is specifically claimed in Claim 27(a)"  
FT 192..202 /note= "penultimate strand region"  
FT 214..218 /note= "WSXWS motif"  
FT 238..255 /note= "transmembrane domain"  
FT 256..538 /note= "intracellular signalling domain; a polypeptide comprising this domain is specifically claimed in Claim 27(c)"  
FT 267..273 /note= "Box I signalling site"  
FT 301..304 /note= "Box II signalling site"  
PN WO200017235-A2.  
XX

PD 30-MAR-2000.  
XX 23-SEP-1999; 99WO-US022149.  
XX 23-SEP-1998; 98US-00159254.  
PR 09-MAR-1999; 99US-00265117.  
PR 06-JUL-1999; 99US-00347930.  
XX (ZYMO ) ZYMOGENETICS INC.  
XX Presnell SR, Conklin DC, Novak JE, Hammond AK;  
PI WPI; 2000-292825/25.  
XX N-PSDB; AAZ94533, AAZ94534.  
DR Novel nucleic acid encoding zalphall polypeptide, useful for treating e.g. viral infection or tumors, and for identifying ligands that stimulate cell proliferation.  
XX Claim 27(e); Page 148-149; 190pp; English.  
XX The present sequence is that of zalphall, a novel human class I cytokine receptor that may be involved in an apoptotic cellular pathway, or is a cell-cell signalling molecule, growth factor receptor, or extracellular matrix associated protein with growth factor hormone activity. The sequence was deduced from a cDNA clone (see AAZ94533) isolated from a spinal cord library. Polypeptides comprising amino acids 20-237, 20-255, 256-538, and 1-538 of the present sequence are claimed. Zalphall is expressed in lymph node, peripheral blood leucocytes, spleen and thymus. The mRNA is also abundant in the Raji cell line (ATCC CCL 86) derived from Burkitt's lymphoma. Zalphall polypeptides, and fusion proteins including them, can be obtained by expression in recombinant host cells. They are used: to detect ligands (also ligand agonists and antagonists) that stimulate proliferation and/or development of haematopoietic, lymphoid and myeloid cells, in vitro or in vivo, e.g. as a replacement for serum in culture media; to detect ligand-expressing cancers; to activity (direct antagonists) and to detect ligand-expressing cancers; to raise specific antibodies; and for purification of cognate ligands. Agonistic ligands may stimulate cell-mediated immunity, e.g. for treating (viral) infections associated with immunosuppression, improving the activity of vaccines, suppressing tumours, treating leukaemia and improving T-cell regeneration after bone marrow transplant. Antagonists are useful as immunosuppressants, e.g. in the treatment of autoimmune disease (e.g. rheumatoid arthritis, multiple sclerosis, diabetes), to prevent transplant rejection and to treat T-cell leukemia or lymphoma  
XX Sequence 538 AA;  
Query Match 100.0%; Score 2958; DB 3; Length 538;  
Best Local Similarity 100.0%; Pred. No. 6.2e-240;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MPRGWAAPLLLLLQGGWGPCDLVCYTDYLTQTVICILEMNLHPSTLTLTWQDOYEELKD 60  
DB 1 MPRGWAAPLLLLLQGGWGPCDLVCYTDYLTQTVICILEMNLHPSTLTLTWQDOYEELKD 60  
QY 61 EATCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSCGSGFLAESTKP 120  
DB 61 EATCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSCGSGFLAESTKP 120  
QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRRKLIISYDS 180  
DB 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRRKLIISYDS 180  
QY 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEELKEGWNPHLLL 240  
DB 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEELKEGWNPHLLL 240  
QY 241 LLLLIVVTFPAFWSLKTPLMLKWKIWAQVSPERFPMPLKYGCGSDGPKKVGAPFTGSS 300  
DB 241 LLLLIVVTFPAFWSLKTPLMLKWKIWAQVSPERFPMPLKYGCGSDGPKKVGAPFTGSS 300  
QY 301 LELGWPSEVPSTLEVYSCHPSPRPAKRLQELQEPALVESDCGVPKPSFWPTAQNSSG 360

Db 301 LELGWSPEVSTLEVSCHPRSPAKRLQTELEPAELVESDGVPRKSFPTQNSGG 360  
Qy 361 SAYSEERDRPYGLVSDITVTLDAEGPCTWPCSCDDGYPALDLDALESPSGLEDPLLD 420  
Db 361 SAYSEERDRPYGLVSDITVTLDAEGPCTWPCSCDDGYPALDLDALESPSGLEDPLLD 420  
Qy 421 AGTTVLSCCVSAGSPGLGPGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
Db 421 AGTTVLSCCVSAGSPGLGPGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
Qy 481 FLAGLDMDFDSGFGVSCSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538  
Db 481 FLAGLDMDFDSGFGVSCSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538

RESULT 6  
ID AAB48001 standard; protein; 538 AA.  
XX AAB48001;  
AC AAB48001;  
DT 19-MAR-2001 (first entry)  
DE Human IL-9/IL-2 receptor-like 16445 protein.  
XX Interleukin-9; IL-9; IL-2 receptor; 16445 protein; inflammatory;  
KW T-lymphocyte-related disorder; antiarthritic; antipsoaritic; human;  
KW immunosuppressive; antiaesthetic; antiallergic; antithyroid; cytostatic;  
KW antiarthritic; nephrotropic; gene therapy.  
XX Homo sapiens.

Key Location/Qualifiers  
FH 1..19  
FT Peptide /note= "signal peptide"  
FT Protein 20..538  
FT /note= "mature protein"  
XX WO200069880-A1.  
XX 23-NOV-2000.  
XX 18-MAY-2000; 2000WO-US013687.  
XX 18-MAY-1999; 99US-00313913.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX Hodge MR;  
XX WPI; 2001-016209/02.  
XX N-PSDB; AAC84147.  
XX Novel interleukin-9/interleukin-2 receptor-like polypeptides useful for  
PT diagnosis and treatment of immune, inflammatory and respiratory disorders  
PT and in screening assays for identifying modulators.  
XX Claim 8; Page 104-106; 119pp; English.

The invention relates to isolated human and murine interleukin-9 (IL-9) /IL-2 receptor-like polypeptides. The plasmid containing the encoding cDNA insert is deposited as ATCC PTA-350. The IL-9/IL-2 receptor-like polypeptides (16445 proteins) can be recombinantly produced using standard recombinant methodology. The 16445 proteins are used for identifying their modulators and for diagnosis and treatment of immune, inflammatory and respiratory disorders and disorders associated with lungs, colon, kidney and lymphoid tissues including tonsil and thymus, in particular T-lymphocyte-related disorders including atopic conditions such as asthma, allergy, rheumatoid arthritis, psoriasis, chronic inflammatory diseases and graft versus host disease, disorders involving the colon such as diarrhoea, dysentery, infectious enterocolitis, kidney disorders including polycystic kidney disease, cystic renal dysplasia,

CC disorders of the thymus including lymphomas, Hodgkin disease and  
CC carcinoids. The 16445 polypeptides are also useful as modulating agents  
CC in cellular processes including growth promoting activity, particularly  
CC the antigen-independent proliferation of T-helper cell clones. The  
CC encoding nucleic acid is useful as primers or hybridization probes for  
CC the detection of IL-9/IL-2 receptor-like encoding nucleic acids and for  
CC tissue typing and in forensic biology. The present sequence represents  
CC the human IL-9/IL-2 receptor-like polypeptide (AAH16445)  
XX  
SQ Sequence 538 AA;  
Query Match 100.0%; Score 2958; DB 4; Length 538;  
Best Local Similarity 100.0%; Pred. No. 6.2e-240;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MPRGWAAFLLLLLQGGWGPCDLCVCTDYLTQVICILEMNNLHPSTLTLTWQDQYEELKD 60  
Db 1 MPRGWAAFLLLLLQGGWGPCDLCVCTDYLTQVICILEMNNLHPSTLTLTWQDQYEELKD 60  
Qy 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQECGSLAESIKP 120  
Db 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQECGSLAESIKP 120  
Qy 121 APPENVTVTFSGQYNIWSRSDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRKLISVDS 180  
Db 121 APPENVTVTFSGQYNIWSRSDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRKLISVDS 180  
Qy 181 RSVSLPLLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEBELKGMNPHLL 240  
Db 181 RSVSLPLLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEBELKGMNPHLL 240  
Qy 241 LLLLVIVIPAFWSLTKTHPLWRLMKKIWAVSPERFPMPLKYGCSGDFKKGWGPFTGSS 300  
Db 241 LLLLVIVIPAFWSLTKTHPLWRLMKKIWAVSPERFPMPLKYGCSGDFKKGWGPFTGSS 300  
Qy 301 LELGWSPEVSTLEVSCHPRSPAKRLQTELEPAELVESDGVPRKSFPTQNSGG 360  
Db 301 LELGWSPEVSTLEVSCHPRSPAKRLQTELEPAELVESDGVPRKSFPTQNSGG 360  
Qy 361 SAYSEERDRPYGLVSDITVTLDAEGPCTWPCSCDDGYPALDLDALESPSGLEDPLLD 420  
Db 361 SAYSEERDRPYGLVSDITVTLDAEGPCTWPCSCDDGYPALDLDALESPSGLEDPLLD 420  
Qy 421 AGTTVLSCCVSAGSPGLGPGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
Db 421 AGTTVLSCCVSAGSPGLGPGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
Qy 481 FLAGLDMDFDSGFGVSCSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538  
Db 481 FLAGLDMDFDSGFGVSCSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538

RESULT 7  
AAB81960  
ID ABB81960 standard; protein; 538 AA.  
XX ABB81960;  
AC ABB81960;  
DT 25-NOV-2002 (first entry)  
XX Human 16445 protein.  
DE Human 16445 protein.  
XX Interleukin; IL-9; IL-2; 16445; antiaesthetic; antiallergic; human;  
KW antipsoaritic; antiinflammatory; immunosuppressive; cytostatic; virucide;  
KW antirheumatic; antiarthritic; antidiabetic; antithyroid; dermatological;  
KW nephrotropic; antibacterial; tuberculoostatic; antileprotic; antipyrretic;  
KW antiulcer; gene therapy; receptor.  
XX Homo sapiens.  
XX US2002090680-A1.  
XX 11-JUL-2002.  
PD

XX	26-SEP-2001; 2001US-00965313.	QY	421	AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS	480
XX		Db	421	AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS	480
PR	18-MAY-1999; 99US-00313913.	QY	481	PLAGLDMDTDFSGFVGSDCSPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGPQAS	538
XX	18-MAY-2000; 2000US-00574100.	Db	481	PLAGLDMDTDFSGFVGSDCSPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGPQAS	538
PA	(MILL-) MILLENNIUM PHARM INC.				
XX					
PI	Hodge MR;				
XX					
DR	WPI; 2002-655832/70.	RESULT 8			
DR	N-PSDB; ABQ79536.	AAU11912			
XX		ID	AAU11912	standard; protein; 538 AA.	
XX		XX	XX	AAU11912;	
PT	New interleukin-9/interleukin-2 receptor-like polypeptides and	AC	XX		
PT	polynucleotides for diagnosing, treating respiratory, T-lymphocyte	XX	XX		
PT	related disorders and disorders associated with lung, colon, kidney and	DT	09-APR-2002	(first entry)	
PT	lymphoid tissues.	XX	XX		
XX		XX	XX	Human MU-1 haematopoietin receptor superfamily chain protein sequence.	
PS	Claim 8; Page 31-33; 54pp; English.	DE	XX		
XX		XX	XX	Human; MU-1; haematopoietin receptor superfamily chain; thyroiditis;	
CC	The invention relates to isolated interleukin (IL)-9/IL-2 receptor-like	KW	XX	immune deficiency; anaemia; autoimmune disorder; multiple sclerosis;	
CC	polypeptide, 16445. The 16445 polypeptides can be expressed by standard	KW	XX	systemic lupus erythematosus; rheumatoid arthritis;	
CC	recombinant methodology. The 16445 polypeptide, polynucleotides and their	KW	XX	pulmonary inflammation; insulin dependent diabetes mellitus;	
CC	modulators are useful for modulating the immune, inflammatory and	KW	XX	nutritional supplement; cytokine receptor family.	
CC	respiratory responses, for the diagnosis and treatment of immune and	XX	XX		
CC	respiratory disorders, particularly for the treatment and diagnosis of T-	OS	XX	Homo sapiens.	
CC	lymphocyte-related disorders, including, atopic conditions, such as	XX	XX		
CC	asthma and allergy, including allergic rhinitis, psoriasis, the effects	XX	XX		
CC	of pathogen infection, chronic inflammatory diseases, organ-specific	XX	XX		
CC	autoimmunity, graft rejection, and graft versus host disease. The	XX	XX		
CC	molecules are also useful as modulating agents in a variety of cellular	XX	XX		
CC	processes including growth promoting activity, particularly the antigen	XX	XX		
CC	independent proliferation of T helper cell clones, and direct effects on	XX	XX		
CC	normal haemopoietic progenitors, human T cells, B cells, thymocytes,	XX	XX		
CC	thymic lymphomas and neuronal cell lines. They are useful for the	XX	XX		
CC	modulation, diagnosis, and treatment of immune, inflammatory, and	XX	XX		
CC	respiratory disorders and disorders associated with lungs, colon, kidney,	XX	XX		
CC	and lymphoid tissues including tonsil and thymus. The present sequence	XX	XX		
CC	represents a human 16445 polypeptide	XX	XX		
XX		XX	XX		
SQ	Sequence 538 AA;	XX	XX		
	Query Match 100.0%; Score 2958; DB 5; Length 538;	PI	Donaldson DD, Unger MJ, Young DA, Whitters MJ, Lowe L, Collins M;		
	Best Local Similarity 100.0%; Pred. No. 6.2e-240;	XX	XX		
	Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	WPI; 2002-062239/08.		
		DR	N-PSDB; AAS17248.		
QY	1 MPRGWAAPLLLLLQGGGCPDLVCYDYLTQVTCILEMWNLHPSTLTLTWQDQYEELKD 60	XX	XX	New polypeptide, useful for identifying compounds binding to MU-1, and	
Db	1 MPRGWAAPLLLLLQGGGCPDLVCYDYLTQVTCILEMWNLHPSTLTLTWQDQYEELKD 60	PT	XX	for treating multiple sclerosis, rheumatoid arthritis, diabetes and	
QY	61 EATSCSLHRSANATHATYTCMDVHFHMADDIFSVNITDQSGNYSQEGSFLAESIKP 120	PT	XX	asthma, comprises the isolated murine MU-1 protein, and a hematopoietin	
Db	61 EATSCSLHRSANATHATYTCMDVHFHMADDIFSVNITDQSGNYSQEGSFLAESIKP 120	XX	XX	receptor superfamily chain.	
QY	121 APPFNVTTFSGQYNISRWSDYEDAFYMLKGLQYELQYRNRGDPWAPSPRKLISYDS 180	PS	Disclosure; Fig 4; 59pp; English.		
Db	121 APPFNVTTFSGQYNISRWSDYEDAFYMLKGLQYELQYRNRGDPWAPSPRKLISYDS 180	XX	XX	The present invention relates to a new murine MU-1 protein, a	
QY	181 RVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIPTQSEELKEGWNPHLL 240	CC	XX	haematopoietin receptor superfamily chain, comprising a fully defined	
Db	181 RVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIPTQSEELKEGWNPHLL 240	CC	XX	sequence of 529 amino acids (AAU1915) as given in the specifications or	
QY	241 LLLLIVIFTPAFWSLKTPLWKLKLIWAVSPSPFFMPLYKGCSDGPKWVGAPFTGSS 300	CC	XX	fragment of protein having MU-1 biological activity. The molecules of the	
Db	241 LLLLIVIFTPAFWSLKTPLWKLKLIWAVSPSPFFMPLYKGCSDGPKWVGAPFTGSS 300	CC	XX	invention may exhibit cytokine, cell proliferation or cell	
QY	301 LELGWPSPVPSTLEVYSCHPPRSPAKRLQLTELQEPALVESDGVPPKPSFWPTAQNCGG 360	CC	XX	differentiation activity and may also exhibit immune stimulating or	
Db	301 LELGWPSPVPSTLEVYSCHPPRSPAKRLQLTELQEPALVESDGVPPKPSFWPTAQNCGG 360	CC	XX	immune suppressing activity and can be useful in the treatment of various	
QY	361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLDPLLD 420	CC	XX	immune deficiencies and disorders including severe combined	
Db	361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLDPLLD 420	CC	XX	immunodeficiency (SCID). Another use of the invention is treating	
		CC	XX	autoimmune disorders such as connective tissue disease, multiple	
		CC	XX	sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune	
		CC	XX	pulmonary inflammation, autoimmune thyroiditis, insulin dependent	
		CC	XX	diabetes mellitus, and autoimmune inflammatory eye disease. The invention	
		CC	XX	is useful for the treatment of myeloid or lymphoid cell deficiencies and	
		CC	XX	in treating various anemias or for use in conjunction with	
		CC	XX	irradiation/chemotherapy to stimulate the production of erythroid	
		CC	XX	precursors and/or erythroid cells. The polynucleotides and proteins can	
		CC	XX	also be used as nutritional sources or supplements. The present protein	
		CC	XX	sequence represents the human MU-1 haematopoietin receptor superfamily	



CC chain. MU-1 is also a member of the cytokine receptor family. This  
CC sequence was used in the invention for the characterisation of previously  
CC unknown members of the haematopoietin receptor superfamily  
XX  
SQ Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 5; Length 538;  
Best Local Similarity 100.0%; Pred. No. 6.2e-240; Indels 0; Gaps 0;  
Matches 538; Conservative 0; Mismatches 0;

QY 1 MPRGWAAPLLLLLLQGGWCPDLVCYTDYLTQVTCILEMWNLHPSTLTLTWQDQYEELKD 60  
DB 1 MPRGWAAPLLLLLLQGGWCPDLVCYTDYLTQVTCILEMWNLHPSTLTLTWQDQYEELKD 60  
QY 61 EATSCSLHRSANATHATYTCMDVHFHMADDFSVNITDQSGNYSQEGCSFLAESIKP 120  
DB 61 EATSCSLHRSANATHATYTCMDVHFHMADDFSVNITDQSGNYSQEGCSFLAESIKP 120  
QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRRKLISVDS 180  
DB 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRRKLISVDS 180  
QY 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVIFQTSBELKEGWNPHLLL 240  
DB 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVIFQTSBELKEGWNPHLLL 240  
QY 241 LLLLIVVTFAPFWSLKTPLMLWKKIWAVSPERFFMPLYKGCSDGFKKWVGAPFTGSS 300  
DB 241 LLLLIVVTFAPFWSLKTPLMLWKKIWAVSPERFFMPLYKGCSDGFKKWVGAPFTGSS 300  
QY 301 LELGWSPEVPSTLEYSCHPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSGG 360  
DB 301 LELGWSPEVPSTLEYSCHPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSGG 360  
QY 361 SAYSEERDRPYGLVSTDTVTLLDAEGCTWPCSCDDGYPALDLGALPSPGLDPLLD 420  
DB 361 SAYSEERDRPYGLVSTDTVTLLDAEGCTWPCSCDDGYPALDLGALPSPGLDPLLD 420  
QY 421 AGTTLVSCGCVSAGSFGGLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
DB 421 AGTTLVSCGCVSAGSFGGLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
QY 481 PLAGLDMDTFDSGFGVSDCSSPEVCDFTSPGDEGPPRSYLROWVIPPPLSPFGQAS 538  
DB 481 PLAGLDMDTFDSGFGVSDCSSPEVCDFTSPGDEGPPRSYLROWVIPPPLSPFGQAS 538

RESULT 9

AAE13726  
ID AAE13726 standard; protein; 538 AA.

AAE13726;

26-FEB-2002 (first entry)

Human soluble Zalphall cytokine receptor protein.

Human; Zalphall; cytokine receptor; immunosuppressive; cytostatic;  
inflammatory disorder; haemostatic; cell proliferation; immune disorder;  
autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;  
myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma;  
ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;  
viral infection.

Homo sapiens.

Key Location/Qualifiers

FT Peptide 1..19

FT Protein 20..538 /label= Signal\_peptide

FT Protein /label= Mature\_Zalphall\_protein

FT Domain 20..237

FT /label= Cytokine\_binding\_domain

FT Domain 120..123  
FT /label= Domain\_linker  
FT Region 192..202  
FT /note= "penultimate strand region"  
FT Domain 214..218  
FT /note= "WSXWS motif"  
FT Domain 238..255  
FT /label= Transmembrane\_domain  
FT Domain 256..538  
FT /label= Intracellular\_signalling\_domain  
FT Region 267..273  
FT /note= "Box I signalling site"  
FT Region 301..304  
FT /note= "Box II signalling site"  
FT Binding-site 519..522  
FT /label= STAT3\_binding\_site  
PN WO200177171-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 03-APR-2001; 2001WO-US010872.  
XX 05-APR-2000; 2000US-0194731P.  
XX 28-JUL-2000; 2000US-0222121P.  
XX (ZYMO ) ZYMOGENETICS INC.  
XX  
XX Sprecher CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ;  
WPI, 2002-025898/03.  
XX N-PSDB; AAD22918.  
XX  
XX Novel soluble receptor polypeptides and polynucleotides used as cytokine  
XX antagonist for stimulating ligand activity-induced proliferation of  
XX hematopoietic cells and for suppressing immune response in a mammal.  
PS Example 1; Page 172-173; 243pp; English.  
XX  
XX The invention relates to an isolated soluble zalphall cytokine receptor  
XX polypeptide and their cDNA molecules. Zalphall proteins are useful for  
XX inhibiting or antagonising the ligand activity-induced proliferation of  
XX haematopoietic cells and haematopoietic cell progenitors preferably  
XX lymphoid cells which are natural killer cells or cytotoxic T cells.  
XX Zalphall is useful for treating immune and inflammatory disorders, for  
XX reducing proliferation of neoplastic B or T cells, for suppressing an  
XX immune response in a mammal exposed to an antigen or pathogen. Zalphall is  
XX useful for treating diseases that require immune regulation including  
XX autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,  
XX myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;  
XX asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,  
XX sepsis, viral infection (dengue virus infection) and cancer. The present  
XX sequence is human soluble Zalphall cytokine receptor protein  
SQ Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 5; Length 538;  
Best Local Similarity 100.0%; Pred. No. 6.2e-240;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGWAAPLLLLLLQGGWCPDLVCYTDYLTQVTCILEMWNLHPSTLTLTWQDQYEELKD 60  
DB 1 MPRGWAAPLLLLLLQGGWCPDLVCYTDYLTQVTCILEMWNLHPSTLTLTWQDQYEELKD 60  
QY 61 EATSCSLHRSANATHATYTCMDVHFHMADDFSVNITDQSGNYSQEGCSFLAESIKP 120  
DB 61 EATSCSLHRSANATHATYTCMDVHFHMADDFSVNITDQSGNYSQEGCSFLAESIKP 120  
QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRRKLISVDS 180  
DB 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRRKLISVDS 180  
QY 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVIFQTSBELKEGWNPHLLL 240

Db 181 RSVSLLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLL 240  
Qy 241 LLLLIVITPAFWSLKTPLWRLWKTIWAVSPERFFMPLKYGSGDFKWKVGAPFTGSS 300  
Db 241 LLLLIVITPAFWSLKTPLWRLWKTIWAVSPERFFMPLKYGSGDFKWKVGAPFTGSS 300  
Qy 301 LELGWSPEVPSTLEVYCHPPSPAKRLQLTLEQPAELVESDGVKPSFWPTAQNSSG 360  
Db 301 LELGWSPEVPSTLEVYCHPPSPAKRLQLTLEQPAELVESDGVKPSFWPTAQNSSG 360  
Qy 361 SAYSEERDRPYGLVSDITVTLDAEGPCTWPCSCDDGYPALDLDALESPGLEDPDLD 420  
Db 361 SAYSEERDRPYGLVSDITVTLDAEGPCTWPCSCDDGYPALDLDALESPGLEDPDLD 420  
Qy 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
Db 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
Qy 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 538  
Db 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 538

RESULT 10  
AAU11978  
ID AAU11978 standard; protein; 538 AA.  
XX AAU11978;  
AC AAU11978;  
XX  
DT 09-APR-2002 (first entry)  
XX Human zalphall receptor polypeptide.  
DE  
XX Cytokine; zalphall ligand; zalphall receptor; NK cell progenitor;  
KW natural killer cell proliferation; T-cell proliferation;  
KW B-cell proliferation; anti-tumour response; immune system;  
XX immunostimulant; cytostatic; human.  
Xf  
OS Homo sapiens.  
XX  
PN US6307024-B1.  
XX  
PD 23-OCT-2001.  
XX  
PF 09-MAR-2000; 2000US-00522217.  
XX  
PR 09-MAR-1999; 99US-0123547P.  
PR 11-MAR-1999; 99US-0123904P.  
PR 01-JUL-1999; 99US-0142013P.  
XX  
PA (ZYMO) ZYMOGENETICS INC.  
XX  
PI Novak JE, Preenell SR, Sprecher CA, Foster DC, Holly RD;  
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;  
XX  
DR WPI: 2002-040208/05.  
DR N-PSDB; AAS20642.  
XX  
XX New zalphall ligand polypeptides and polynucleotides, useful for  
PT stimulating proliferation, activation, differentiation and/or induction  
PT of inhibition of specialized cell function, or for stimulating an  
PT antigenic response.  
XX  
PS Claim 1; Col 191-194; 105pp; English.  
XX  
CC The present invention relates to the isolation of a novel cytokine,  
CC zalphall ligand and the polynucleotide encoding it. The invention also  
CC gives the sequence for the zalphall receptor and the polynucleotide  
CC encoding it. The zalphall ligand polypeptide stimulates proliferation of  
CC natural killer (NK) cells or NK cell progenitors, the activation of NK  
CC cells, proliferation of T-cells, proliferation of B-cells stimulated with  
CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and

CC reduces proliferation of B-cells stimulated with anti-IgM antibodies. The  
CC zalphall ligand polypeptide is also useful in preparing antibodies that  
CC bind to zalphall Ligand epitopes. The zalphall Ligand polynucleotides can  
CC be used as probes or primers to clone regions of a zalphall Ligand gene,  
CC and in gene therapy. Zalphall Ligand may also be used to identify  
CC inhibitors of its activity, to enhance the generation of anti-tumour  
CC responses with or without the infusion of donor lymphocytes, and to  
CC activate or stimulate the immune system. The present sequence represents  
XX human zalphall receptor polypeptide  
SQ Sequence 538 AA;  
Query Match 100.0%; Score 2958; DB 5; Length 538;  
Best Local Similarity 100.0%; Pred. No. 6.2e-240;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MPRGWAAPLLLLLLQGGWGPCDLVCTDYDTQVTCILEMNLHPSTLTLTWQDQYEELKD 60  
Db 1 MPRGWAAPLLLLLLQGGWGPCDLVCTDYDTQVTCILEMNLHPSTLTLTWQDQYEELKD 60  
Qy 61 EATSCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQCSFLLAEIKP 120  
Db 61 EATSCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQCSFLLAEIKP 120  
Qy 121 APPENVTVTFSGQYNIISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRKLISVDS 180  
Db 121 APPENVTVTFSGQYNIISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRKLISVDS 180  
Qy 181 RVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLL 240  
Db 181 RVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLL 240  
Qy 241 LLLLIVITPAFWSLKTPLWRLWKTIWAVSPERFFMPLKYGSGDFKWKVGAPFTGSS 300  
Db 241 LLLLIVITPAFWSLKTPLWRLWKTIWAVSPERFFMPLKYGSGDFKWKVGAPFTGSS 300  
Qy 301 LELGWSPEVPSTLEVYCHPPSPAKRLQLTLEQPAELVESDGVKPSFWPTAQNSSG 360  
Db 301 LELGWSPEVPSTLEVYCHPPSPAKRLQLTLEQPAELVESDGVKPSFWPTAQNSSG 360  
Qy 361 SAYSEERDRPYGLVSDITVTLDAEGPCTWPCSCDDGYPALDLDALESPGLEDPDLD 420  
Db 361 SAYSEERDRPYGLVSDITVTLDAEGPCTWPCSCDDGYPALDLDALESPGLEDPDLD 420  
Qy 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
Db 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
Qy 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 538  
Db 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 538

RESULT 11  
ABR61402  
ID ABR61402 standard; protein; 538 AA.  
XX ABR61402;  
AC ABR61402;  
XX  
DT 12-AUG-2003 (first entry)  
XX  
DE Human IL-21R SEQ ID NO:2.  
XX  
KW arthritic disorder; interleukin-21; IL-21; IL-21 receptor; IL-21R;  
KW immune cell activity; cancer; infectious disorder; antirheumatic;  
KW ankylosing spondylitis; osteoporosis; antipsoriatic; cytostatic; antibacterial;  
KW virucide; antiparasitic; immunosuppressive; antidiabetic; dermatological;  
KW neuroprotective; antiulcer; antiallergic; antianemic; hepatotropic;  
KW antithyroid; antiinflammatory; immune response; immune disorder;  
KW autoimmune disease; human.  
XX  
OS Homo sapiens.  
XX

PN WO2003028630-A2.  
 PP 10-APR-2003.  
 PF 04-OCT-2002; 2002WO-US029839.  
 PP 04-OCT-2001; 2001US-00972218.  
 PR 17-APR-2002; 2002US-0373746P.  
 XX (AMHP ) WYETH.  
 PA Carter L, Whitters MJ, Collins M, Young DA, Larsen G;  
 PI Donaldson DD, Lowe LD, Dunussi K, Ma M, Witek JS, Kasaian MT;  
 PI Ungar M;  
 XX WPI; 2003-430146/40.  
 DR N-PSDB; ACC80861.  
 XX  
 PT Treating or preventing arthritic disorder, cancer or infectious disorders  
 PT in a subject, involves administering a modulator of interleukin-21 or its  
 PT receptor which modulate immune cell activity.  
 XX  
 PS Claim 40; Fig 2B; 176pp; English.  
 XX  
 CC The invention relates to a novel method for treating or preventing an  
 CC arthritic disorder in a subject. The method involves administering to the  
 CC subject an interleukin-21 (IL-21)/IL-21 receptor (IL-21R) antagonist  
 CC optionally in combination with another therapeutic agent, to inhibit or  
 CC reduce immune cell activity in the subject. The method is also useful for  
 CC treating or preventing cancer or an infectious disorder, in a subject, by  
 CC administering IL-21/IL-21R agonist, to increase immune cell activity. The  
 CC method of the invention has antirheumatic, antiarthritic, osteopathic,  
 CC antipsoriatic, cycostatic, antibacterial, virucide, antiparasitic,  
 CC immunosuppressive, antidiabetic, neuroprotective, dermatological,  
 CC antitumor, antiallergic, antianemic, hepatotropic,  
 CC antithyroid, and antiinflammatory activity. The method is useful for  
 CC treating or preventing an arthritic disorder such as rheumatoid  
 CC arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic  
 CC arthritis or ankylosing spondylitis, and also cancer such as solid  
 CC tumour, soft tissue tumour or metastatic lesion, or an infectious  
 CC disorder such a bacterial, viral or parasitic infection in a mammal,  
 CC preferably human. A method of the invention is also useful for  
 CC increasing the ability of a vaccine composition containing an antigen to  
 CC elicit a protective immune response in a subject against the antigens.  
 CC The antigen is from a pathogen such as virus, bacterium or protozoan, or  
 CC from cancer or tumour cell antigen, or expressed on the surface of cancer  
 CC cell. An alternative method of the invention is useful for modulating the  
 CC activity of immune or haematopoietic cells and thus to treat or prevent a  
 CC variety of immune disorders, such as autoimmune diseases, for example  
 CC diabetes mellitus, multiple sclerosis, myasthenia gravis, systemic lupus  
 CC erythematosus, dermatitis, ulcer, asthma, allergic asthma, anaemia,  
 CC hepatitis, Graves's disease, graft versus host disease, and scleroderma.  
 CC The present sequence is used in an exemplification of the invention  
 XX  
 SQ Sequence 538 AA;  
 Query Match 100.0%; Score 2958; DB 6; Length 538;  
 Best Local Similarity 100.0%; Pred. NO. 6.2e-240;  
 Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MPRGWAAPLLLLLGGGCGPDLVCYTDYLTQVTCILEMWNLPSTLTITWQDYELKD 60  
 DB 1 MPRGWAAPLLLLLGGGCGPDLVCYTDYLTQVTCILEMWNLPSTLTITWQDYELKD 60  
 QY 61 EATSCSLHRSANATHATYTCMDVPHFWADDIFSVNITDQSGNTSQEGSFLLAESIKP 120  
 DB 61 EATSCSLHRSANATHATYTCMDVPHFWADDIFSVNITDQSGNTSQEGSFLLAESIKP 120  
 QY 121 APPFNVTTFSGQYNISWSDYEDPAFYMLKGLQYELQYRNRPWAVSPRKLISVDS 180  
 DB 121 APPFNVTTFSGQYNISWSDYEDPAFYMLKGLQYELQYRNRPWAVSPRKLISVDS 180  
 QY 181 RSVSLLPLEFRKDDSSYELQVRAGMPGSSYQGTWSENSDPVTFQTSSELKEGWNPHLLL 240

DB 181 RSVSLLPLEFRKDDSSYELQVRAGMPGSSYQGTWSENSDPVTFQTSSELKEGWNPHLLL 240  
 QY 241 LLLLVIVFIPAFWSLKTHPLMRLWKKIWAVSPERFFMPLYKGCSDGFKKWWGAPFTGSS 300  
 DB 241 LLLLVIVFIPAFWSLKTHPLMRLWKKIWAVSPERFFMPLYKGCSDGFKKWWGAPFTGSS 300  
 QY 301 LELGWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTQNSGG 360  
 DB 301 LELGWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTQNSGG 360  
 QY 361 SAYSERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLGDEPLLD 420  
 DB 361 SAYSERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLGDEPLLD 420  
 QY 421 AGTTVLSGCVSAGSPGLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGVSEAGS 480  
 DB 421 AGTTVLSGCVSAGSPGLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGVSEAGS 480  
 QY 481 PLAGLDMDTFDSGFGVSDCSSPVCECDFTSPGDEGPRSVILQWVITPPPLSSPGPQAS 538  
 DB 481 PLAGLDMDTFDSGFGVSDCSSPVCECDFTSPGDEGPRSVILQWVITPPPLSSPGPQAS 538  
 RESULT 12  
 AAEI4939  
 ID AAEI4939 standard; protein; 538 AA.  
 AC AAEI4939;  
 DT 27-AUG-2003 (first entry)  
 XX Human interleukin-21 (IL-21) receptor.  
 DE Interleukin-21; antagonist; cancer; inflammatory; autoimmune disorder;  
 KW rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;  
 KW myasthenia gravis; diabetes; human; zalphall receptor; IL-21 receptor.  
 XX Homo sapiens.  
 OS WO2003040313-A2.  
 PN 15-MAY-2003.  
 PD 28-OCT-2002; 2002WO-US034502.  
 PF 05-NOV-2001; 2001US-0337586P.  
 PR (ZYMO ) ZYMOGENETICS INC.  
 PA Presnell SR, West JW, Novak JE;  
 PI WPI; 2003-441547/41.  
 DR N-PSDB; AAD47859.  
 XX  
 PT New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing  
 PT and treating disorders with aberrant expression or activity of the IL-21  
 PT polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and  
 PT diabetes.  
 XX Example 1; Page 65-67; 71pp; English.  
 PS The invention relates to polynucleotides and polypeptides of interleukin-  
 CC 21 (IL-21) antagonists, that bind with specificity and exhibit an EC50  
 CC that is not detectable in receptor binding studies. The antagonists of  
 CC the invention have mutations in the D helix of the IL-21 molecule, and  
 CC can be used to inhibit the activity of IL-21 with its cognate receptor.  
 CC The IL-21 antagonists are useful for diagnosing and treating disorders  
 CC involving the aberrant expression or activity of the IL-21 polypeptide,  
 CC such as cancer, inflammatory and autoimmune disorders, including  
 CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,  
 CC myasthenia gravis and diabetes. The polypeptides can also be used to  
 CC prepare antibodies that bind IL-21 epitopes, peptides or polypeptides,

CC and for enhancing in vivo killing of target tissues. The present sequence  
 CC is human IL-21 receptor (originally designated zalpha11 receptor)

SQ Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 7; Length 538;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-240;  
 Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGWAAPLLLLLLQGGWGPCDLYCYTDYLTQVICILEMNNLHPSTLTLTWQDQVEELKD 60  
 DB 1 MPRGWAAPLLLLLLQGGWGPCDLYCYTDYLTQVICILEMNNLHPSTLTLTWQDQVEELKD 60

QY 61 EATCSLHRSAHNATHATYTCMDVDFHFMADDFSVNITDQSGNYSCGCSFLLAESIKP 120  
 DB 61 EATCSLHRSAHNATHATYTCMDVDFHFMADDFSVNITDQSGNYSCGCSFLLAESIKP 120

QY 121 APPFNVTTFSGQYNIWSRDYEDPAFYMLKGKQLQYELQYRNRPDPAVSPRRKLISVDS 180  
 DB 121 APPFNVTTFSGQYNIWSRDYEDPAFYMLKGKQLQYELQYRNRPDPAVSPRRKLISVDS 180

QY 181 RVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEELKEGWNPHLLL 240  
 DB 181 RVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEELKEGWNPHLLL 240

QY 241 LLLLVIPTPAFWSLTKTHPLWRLWKIWA VSPERFFMPLKYKCGSDFKKVGAPFTGSS 300  
 DB 241 LLLLVIPTPAFWSLTKTHPLWRLWKIWA VSPERFFMPLKYKCGSDFKKVGAPFTGSS 300

QY 301 LELGWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQNCGG 360  
 DB 301 LELGWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQNCGG 360

QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSFGLDPLLD 420  
 DB 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSFGLDPLLD 420

QY 421 AGTTVLSCGCVSAGSPGLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
 DB 421 AGTTVLSCGCVSAGSPGLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480

QY 481 FLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGQAS 538  
 DB 481 FLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGQAS 538

RESULT 13

ID ABU62888  
 AC ABU62888 standard; protein; 538 AA.  
 AC ABU62888;  
 DT 15-SEP-2003 (first entry)  
 DE Human MU-1 haematopoietin receptor superfamily chain.  
 DE Human; MU-1; haematopoietin receptor superfamily chain; immunomodulator;  
 KW cytostatic; antibacterial; virucide; antianaemic; gene therapy;  
 KW haematopoiesis; anaemias; immune response; cancer; infection;  
 KW transplanted organ; cytokine; receptor.  
 XX Homo sapiens.  
 XX US2003049798-A1.  
 XX 13-MAR-2003.  
 XX 04-OCT-2001; 2001US-00972218.  
 XX 17-MAR-1998; 98US-00040005.  
 XX 28-APR-2000; 2000US-00560766.  
 XX 11-MAY-2000; 2000US-00569384.  
 XX

(CART/) CARTER L.  
 (WHIT/) WHITTERS M J.  
 (COLL/) COLLINS M.  
 (YOUN/) YOUNG D A.  
 (DONA/) DONALDSON D D.  
 (LOWE/) LOWE L D.  
 (UNGE/) UNGER M.

Carter L, Whitters MJ, Collins M, Young DA, Donaldson DD;  
 Lowe LD, Unger M;

WPI; 2003-512354/48.  
 N-PSDB; ACD26717.

New fusion polypeptide for regulating hematopoiesis and immune responses,  
 comprises a fragment of a MU-1 polypeptide and a non-MU-1 fusion  
 polypeptide.

Claim 13; Fig 4; 26pp; English.

The invention describes a fusion polypeptide comprising at least a  
 fragment of a MU-1 polypeptide and a non-MU-1 fusion polypeptide. The  
 polypeptide is useful in regulating haematopoiesis (e.g. in cases of  
 anaemias) and/or immune responses (e.g. immune response to cancer,  
 infections or to a transplanted organ) and in identifying other members  
 of the haematopoietin superfamily, including cytokines and receptors. The  
 polynucleotide may be used to express recombinant protein for analysis,  
 characterisation or therapeutic use; and as markers for tissues or  
 chromosomes. The polypeptide and polynucleotide may also be used as  
 nutritional sources or supplements. This is the amino acid sequence of  
 human MU-1 haematopoietin receptor superfamily chain

Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 7; Length 538;

Best Local Similarity 100.0%; Pred. No. 6.2e-240;

Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGWAAPLLLLLLQGGWGPCDLYCYTDYLTQVICILEMNNLHPSTLTLTWQDQVEELKD 60  
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QY 121 APPFNVTTFSGQYNIWSRDYEDPAFYMLKGKQLQYELQYRNRPDPAVSPRRKLISVDS 180  
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QY 181 RVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEELKEGWNPHLLL 240  
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QY 241 LLLLVIPTPAFWSLTKTHPLWRLWKIWA VSPERFFMPLKYKCGSDFKKVGAPFTGSS 300  
 DB 241 LLLLVIPTPAFWSLTKTHPLWRLWKIWA VSPERFFMPLKYKCGSDFKKVGAPFTGSS 300

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 DB 301 LELGWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQNCGG 360

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QY 421 AGTTVLSCGCVSAGSPGLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
 DB 421 AGTTVLSCGCVSAGSPGLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480

QY 481 FLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGQAS 538  
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ID ABW00881 standard; protein; 538 AA.  
XX  
AC ABW00881;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human cytokine receptor, Zalphall protein.  
XX  
KW Cytokine receptor; Zalphall; cell proliferation; cell development;  
KW splenic disorder; blood disorder; bone disorder; immune disorder;  
KW haematopoietic; lymphoid; inflammatory; therapy; receptor; human.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT Protein 20..538 /label= Signal\_peptide  
FT Binding-site 20..237 /note= "Mature human Zalphall protein"  
FT Region 120..123 /note= "Cytokine-binding domain"  
FT Region 192..202 /note= "Domain linker"  
FT Domain 214..218 /note= "Penultimate strand region"  
FT Domain 238..255 /note= "WSXWS motif"  
FT Domain 256..538 /note= "Transmembrane domain"  
FT Region 267..273 /note= "Intracellular signalling domain"  
FT Region 301..304 /note= "Box I signalling site"  
FT /note= "Box II signalling site"  
XX  
PN US6576744-B1.  
XX  
PD 10-JUN-2003.  
XX  
PF 23-SEP-1999; 99US-00404641.  
XX  
PR 23-SEP-1998; 98US-0100896P.  
PR 09-MAR-1999; 99US-0123546P.  
PR 06-JUL-1999; 99US-0142574P.  
XX  
PA (ZYMO ) ZYMOGENETICS INC.  
XX  
PI Presnell SR, Conklin DC, Novak JE, Hammond AK;  
XX  
DR WPI; 2003-799829/75.  
DR N-PSDB; AAD61882.  
XX  
PT Novel cytokine receptor Zalphall useful for treating lymphoid, immune,  
PT inflammatory, splenic, blood or bone disorders.  
XX  
PS Claim 1; Fig 2; Opp; English.  
XX  
CC The invention relates to a cytokine receptor designated Zalphall and its  
CC nucleic acid sequence. Zalphall protein is useful for detecting ligands  
CC that stimulate the proliferation and/or development of haematopoietic,  
CC lymphoid and myeloid cells in vitro and in vivo. Zalphall DNA is useful  
CC in identifying a region of the genome associated with human disease  
CC states. Zalphall protein is useful for treating lymphoid, immune,  
CC inflammatory, splenic, blood or bone disorders. The present sequence is  
XX human Zalphall protein  
XX  
SQ Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 7; Length 538;  
Best Local Similarity 100.0%; Pred. No. 6.2e-240; Mismatches 0; Indels 0; Gaps 0;  
Matches 538; Conservative 0;  
QY 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLOTVICILEMWNLHPSTLTLTWQDOQEELKD 60  
DB 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLOTVICILEMWNLHPSTLTLTWQDOQEELKD 60  
QY 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSEQCGSFLLAESIKP 120  
DB 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSEQCGSFLLAESIKP 120  
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QY 181 RSVSLLPLEFRKDSSEYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL 240  
DB 181 RSVSLLPLEFRKDSSEYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL 240  
QY 241 LLLLIVIFIPAFWSLKTHPLWRLWKIWA VSPERFFMPLYKGCSDGFKKWWGAPFTGSS 300  
DB 241 LLLLIVIFIPAFWSLKTHPLWRLWKIWA VSPERFFMPLYKGCSDGFKKWWGAPFTGSS 300  
QY 301 LELGWSPEVPSTLEVSCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSSG 360  
DB 301 LELGWSPEVPSTLEVSCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSSG 360  
QY 361 SAYSEERDRPYGLVSDITVTVDAGPCTWPCSCDDGYPALDL DAGLEPSPGLEDP LLD 420  
DB 361 SAYSEERDRPYGLVSDITVTVDAGPCTWPCSCDDGYPALDL DAGLEPSPGLEDP LLD 420  
QY 421 AGTTVLSGCVSAGSPGLGSLDLLKPLPADGEDWAGGLPWGGRSPGVSSEAGS 480  
DB 421 AGTTVLSGCVSAGSPGLGSLDLLKPLPADGEDWAGGLPWGGRSPGVSSEAGS 480  
QY 481 PLAGLDMTDFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538  
DB 481 PLAGLDMTDFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538  
RESULT 15  
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ID ADG87460 standard; protein; 538 AA.  
XX  
AC ADG87460;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Human zalphall protein.  
XX  
KW zalphall; anaemia; human; gene therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT Protein 20..538 /label= Signal\_peptide  
FT Domain 20..237 /note= "Human mature zalphall protein"  
FT Region 120..123 /note= "Cytokine binding domain"  
FT Region 192..202 /note= "Domain linker"  
FT Domain 238..255 /note= "Penultimate strand region"  
FT Domain 256..538 /note= "Transmembrane domain"  
FT Region 267..273 /note= "Complete intracellular signaling domain"  
FT Region 301..304 /note= "Box I signaling site"

FT /note= "Box II signaling site"  
XX US2003148447-A1.  
PN  
XX  
PD 07-AUG-2003.  
XX  
PF 13-SEP-2002; 2002US-00243072.  
XX  
PR 28-JUL-2000; 2000US-00628127.  
XX  
PA (ZYMO ) ZYMOGENETICS INC.  
XX  
XX Presnell SR, Conklin DC, Novak JE, Hammond AK;  
XX  
XX WPI: 2003-897570/82.  
DR N-PSDB; ADG87459.  
XX  
XX New polynucleotide, useful for preparing a composition for treating e.g.,  
PT anemia encodes a zalphall polypeptide cytokine receptor.  
XX  
XX Claim 1; SEQ ID NO 2; 91pp; English.  
XX  
XX The present invention relates to new isolated polynucleotide encoding  
CC zalphall polypeptide. The polynucleotide is useful for treating anaemia.  
CC The invention is useful for producing zalphall polypeptide and producing  
CC an antibody to zalphall polypeptide. The present sequence is human  
CC zalphall protein.  
XX  
XX  
SQ Sequence 538 AA;  
Query Match 100.0%; Score 2958; DB 7; Length 538;  
Best Local Similarity 100.0%; Pred. No. 6.2e-240;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MPRGWAAPLLLLLGGGCGPDLVCYTDYLTQVICILEMWNLHPSTLTWTQDQYEELKD 60  
Db |  
1 MPRGWAAPLLLLLGGGCGPDLVCYTDYLTQVICILEMWNLHPSTLTWTQDQYEELKD 60  
QY 61 EATSCSLHRSANATHATYCHMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120  
Db |  
61 EATSCSLHRSANATHATYCHMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120  
QY 121 APPFNVTTFSCQYNISWRSYEDPAFYMLKGKQLQYELQYRNRGDPWAVSPRKLISVDS 180  
Db |  
121 APPFNVTTFSCQYNISWRSYEDPAFYMLKGKQLQYELQYRNRGDPWAVSPRKLISVDS 180  
QY 181 RVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVIQTQSSEELKEGWNPHLLL 240  
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181 RVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVIQTQSSEELKEGWNPHLLL 240  
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241 LLLLVIPTPAFWSLTKTHPLWELWKKIWAVPSPERFEMPLYKGCSDGFKKWWGAPFTGSS 300  
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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: July 9, 2005, 11:47:11 ; Search time 163 Seconds  
(without alignments)  
1275.127 Million cell updates/sec

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Perfect score: 2958  
Sequence: 1 MPRGWAAFLLLLLQGGWGC.....YLRQWVIPPPLSPGPOAS 538

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Searched: 1726216 seqs, 386330316 residues

Total number of hits satisfying chosen parameters: 1726216

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2958	100.0	538	9	US-09-923-246-115
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4	2958	100.0	538	10	US-09-972-218A-2
5	2958	100.0	538	14	US-10-264-634-2
6	2958	100.0	538	14	US-10-295-723-115
7	2958	100.0	538	14	US-10-282-622-16
8	2958	100.0	538	14	US-10-243-072-2
9	2958	100.0	538	14	US-10-414-186-2
10	2958	100.0	538	15	US-10-456-780-6
11	2958	100.0	538	16	US-10-659-684-115

12	2958	100.0	538	16	US-10-620-169-4
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18	2958	100.0	538	17	US-10-951-239-10
19	2951	99.8	538	9	US-09-758-664-2
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37	1729.5	58.5	529	15	US-10-624-044-6
38	1729.5	58.5	529	18	US-10-415-440-6
39	1591	53.8	289	9	US-09-941-973-2
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ALIGNMENTS

RESULT 1  
US-09-965-313-2  
; Sequence 2, Application US/09965313  
; Patent No. US20020090680A1  
; GENERAL INFORMATION:  
; APPLICANT: Hodge, Martin R.  
; TITLE OF INVENTION: IL-9/IL-2 Receptor-Like Molecules and Uses Thereof  
; FILE REFERENCE: 5800-17A  
; CURRENT APPLICATION NUMBER: US/09/965,313  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: US 09/313,913  
; PRIOR FILING DATE: 1999-05-18  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens IL-2/IL-9 Receptor Like  
US-09-965-313-2

Query Match	100.0%	Score	2958	DB	9	Length	538
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Matches	538	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
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DB	1	MPRGWAAFLLLLLQGGWGC	PDLVCYTDYLTQTVICILEMNLHPSTLTLTWDDQYEE	LD	60		
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DB	61	EATSCSLHRSAHNATHATYTC	CHMDVFFHFMADDIFSVNITD	OSGNSQCSGFLAESIKP	120		
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QY 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
Db 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
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## RESULT 2

US-09-923-246-115  
; Sequence 115, Application US/09923246  
; Patent No. US20020128446A1  
; GENERAL INFORMATION:  
; APPLICANT: No. US20020128446A1ak, Julia E.  
; APPLICANT: Preenell, Scott R.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Gross, Jane A.  
; APPLICANT: Johnston, Janet V.  
; APPLICANT: Nelson, Andrew J.  
; APPLICANT: Dillon, Stacey R.  
; APPLICANT: Hammond, Angela K.  
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND  
; FILE REFERENCE: 99-16  
; CURRENT APPLICATION NUMBER: US/09/923,246  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 2000-03-09  
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01  
; NUMBER OF SEQ ID NOS: 115  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 115  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-923-246-115

Query Match 100.0%; Score 2958; DB 9; Length 538;  
Best Local Similarity 100.0%; Pred. No. 2.3e-228;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGWAAPLLLLLQGGWGPCDLVCYTDYLTQTVICILEMNNLHPSTLTITWQDQYEELKD 60  
Db 1 MPRGWAAPLLLLLQGGWGPCDLVCYTDYLTQTVICILEMNNLHPSTLTITWQDQYEELKD 60  
QY 61 EATSCSLHRSANNAHATYTCMDVHFHMADDIFSVNITDQSGNYSECGSFLAESIKP 120  
Db 61 EATSCSLHRSANNAHATYTCMDVHFHMADDIFSVNITDQSGNYSECGSFLAESIKP 120

QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLOQYLRNRGDPWAVSPRRKLISVDS 180  
Db 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLOQYLRNRGDPWAVSPRRKLISVDS 180  
QY 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVI FQTQSEBELKEGWNPHLLL 240  
Db 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVI FQTQSEBELKEGWNPHLLL 240  
QY 241 LLLLIVIFIPAFWSLKTPLRLWKKIWAVSPERFPMPLYKGCSDGDFKKWVGAPFTGSS 300  
Db 241 LLLLIVIFIPAFWSLKTPLRLWKKIWAVSPERFPMPLYKGCSDGDFKKWVGAPFTGSS 300  
QY 301 LELGPMSPVEPSTLKVYSCHPSPRSPAKRLQTLQEPALVESDGVKXPSFWPTAQNSSG 360  
Db 301 LELGPMSPVEPSTLKVYSCHPSPRSPAKRLQTLQEPALVESDGVKXPSFWPTAQNSSG 360  
QY 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDLDAGLEPSGLEDPLLD 420  
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDLDAGLEPSGLEDPLLD 420  
QY 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
Db 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
QY 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPQAS 538  
Db 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPQAS 538

## RESULT 3

US-09-825-561A-2  
; Sequence 2, Application US/09825561A  
; Patent No. US20020137677A1  
; GENERAL INFORMATION:  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: No. US20020137677A1ak, Julia E.  
; APPLICANT: West, James W.  
; APPLICANT: Preenell, Scott R.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Nelson, Andrew J.  
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS  
; FILE REFERENCE: 00-22  
; CURRENT APPLICATION NUMBER: US/09/825,561A  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/194,731  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/222,121  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 86  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-825-561A-2

Query Match 100.0%; Score 2958; DB 9; Length 538;  
Best Local Similarity 100.0%; Pred. No. 2.3e-228;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGWAAPLLLLLQGGWGPCDLVCYTDYLTQTVICILEMNNLHPSTLTITWQDQYEELKD 60  
Db 1 MPRGWAAPLLLLLQGGWGPCDLVCYTDYLTQTVICILEMNNLHPSTLTITWQDQYEELKD 60  
QY 61 EATSCSLHRSANNAHATYTCMDVHFHMADDIFSVNITDQSGNYSECGSFLAESIKP 120  
Db 61 EATSCSLHRSANNAHATYTCMDVHFHMADDIFSVNITDQSGNYSECGSFLAESIKP 120  
QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLOQYLRNRGDPWAVSPRRKLISVDS 180  
Db 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLOQYLRNRGDPWAVSPRRKLISVDS 180  
QY 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVI FQTQSEBELKEGWNPHLLL 240

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Db 181 RVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVIQTQSEBELKEGWNPHLLL 240
Qy 241 LLLLVIPIPAFWSLKTPLRLWKKIWAVSPERFPMPLKGCSDGDFKWKWGAPFTGSS 300
Db 241 LLLLVIPIPAFWSLKTPLRLWKKIWAVSPERFPMPLKGCSDGDFKWKWGAPFTGSS 300
Qy 301 LELGWSPEVPSTLEVISCHPPSPAKRLQLTELQEPABELVEDSGVPKPSFWPTAQNCGG 360
Db 301 LELGWSPEVPSTLEVISCHPPSPAKRLQLTELQEPABELVEDSGVPKPSFWPTAQNCGG 360
Qy 361 SAYSEERDRPYGLVSTDTVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLLD 420
Db 361 SAYSEERDRPYGLVSTDTVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLLD 420
Qy 421 AGTTVLSCGCVSAGSAGPLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGGVSSEAGS 480
Db 421 AGTTVLSCGCVSAGSAGPLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGGVSSEAGS 480
Qy 481 PLAGLDMOTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLROWVVIPIPLSSFGPQAS 538
Db 481 PLAGLDMOTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLROWVVIPIPLSSFGPQAS 538
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## RESULT 4

US-09-972-218A-2

; Sequence 2, Application US/09972218A

; Publication No. US20030049798A1

; GENERAL INFORMATION:

; APPLICANT: Carter, Laura

; APPLICANT: Whitters, Matthew J

; APPLICANT: Collins, Mary

; APPLICANT: Young, Deborah A.

; APPLICANT: Donaldson, Debra D.

; APPLICANT: Lowe, Leslie D.

; APPLICANT: Unger, Michelle

; TITLE OF INVENTION: MU-1, Member of the Cytokine Receptor Family

; FILE REFERENCE: 22058-552CIP2

; CURRENT APPLICATION NUMBER: US/09/972,218A

; CURRENT FILING DATE: 2002-08-19

; PRIOR APPLICATION NUMBER: 09/569384

; PRIOR FILING DATE: 2000-05-11

; PRIOR APPLICATION NUMBER: 09/560766

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US/6057128

; PRIOR FILING DATE: 1998-03-17

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 2

; LENGTH: 538

; TYPE: PRT

; ORGANISM: Human

US-09-972-218A-2

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Query Match 100.0%; Score 2958; DB 10; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.3e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MPRGWAAPLLLLLLOGGWCPCDPLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60
Db 1 MPRGWAAPLLLLLLOGGWCPCDPLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60
Qy 61 EATCSLHRSANATHATYTCMDVHFHMADDIFSVNITDQSGNYSQECGSLLAESIKP 120
Db 61 EATCSLHRSANATHATYTCMDVHFHMADDIFSVNITDQSGNYSQECGSLLAESIKP 120
Qy 121 APPFNVTTFSGOYNISWRSDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRKLISVDS 180
Db 121 APPFNVTTFSGOYNISWRSDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRKLISVDS 180
Qy 181 RVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVIQTQSEBELKEGWNPHLLL 240
Db 181 RVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVIQTQSEBELKEGWNPHLLL 240
```

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Qy 241 LLLLVIPIPAFWSLKTPLRLWKKIWAVSPERFPMPLKGCSDGDFKWKWGAPFTGSS 300
Db 241 LLLLVIPIPAFWSLKTPLRLWKKIWAVSPERFPMPLKGCSDGDFKWKWGAPFTGSS 300
Qy 301 LELGWSPEVPSTLEVISCHPPSPAKRLQLTELQEPABELVEDSGVPKPSFWPTAQNCGG 360
Db 301 LELGWSPEVPSTLEVISCHPPSPAKRLQLTELQEPABELVEDSGVPKPSFWPTAQNCGG 360
Qy 361 SAYSEERDRPYGLVSTDTVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLLD 420
Db 361 SAYSEERDRPYGLVSTDTVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLLD 420
Qy 421 AGTTVLSCGCVSAGSAGPLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGGVSSEAGS 480
Db 421 AGTTVLSCGCVSAGSAGPLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGGVSSEAGS 480
Qy 481 PLAGLDMOTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLROWVVIPIPLSSFGPQAS 538
Db 481 PLAGLDMOTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLROWVVIPIPLSSFGPQAS 538
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## RESULT 5

US-10-264-634-2

; Sequence 2, Application US/10264634

; Publication No. US20030108549A1

; GENERAL INFORMATION:

; APPLICANT: Donaldson, Debra et al.

; TITLE OF INVENTION: Methods and Compositions for Modulating Interleukin-21 Receptor

; FILE REFERENCE: G15320-P3

; CURRENT APPLICATION NUMBER: US/10/264,634

; CURRENT FILING DATE: 2002-10-04

; PRIOR APPLICATION NUMBER: 09/040,005

; PRIOR FILING DATE: 1998-03-17

; PRIOR APPLICATION NUMBER: 09/560,766

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 09/569,384

; PRIOR FILING DATE: 2000-05-11

; PRIOR APPLICATION NUMBER: 09/972,218

; PRIOR FILING DATE: 2001-10-04

; PRIOR APPLICATION NUMBER: 60/373,746

; PRIOR FILING DATE: 2002-04-17

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 2

; LENGTH: 538

; TYPE: PRT

; ORGANISM: Human

US-10-264-634-2

```
Query Match 100.0%; Score 2958; DB 14; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.3e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MPRGWAAPLLLLLLOGGWCPCDPLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60
Db 1 MPRGWAAPLLLLLLOGGWCPCDPLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60
Qy 61 EATCSLHRSANATHATYTCMDVHFHMADDIFSVNITDQSGNYSQECGSLLAESIKP 120
Db 61 EATCSLHRSANATHATYTCMDVHFHMADDIFSVNITDQSGNYSQECGSLLAESIKP 120
Qy 121 APPFNVTTFSGOYNISWRSDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRKLISVDS 180
Db 121 APPFNVTTFSGOYNISWRSDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRKLISVDS 180
Qy 181 RVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVIQTQSEBELKEGWNPHLLL 240
Db 181 RVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVIQTQSEBELKEGWNPHLLL 240
Qy 241 LLLLVIPIPAFWSLKTPLRLWKKIWAVSPERFPMPLKGCSDGDFKWKWGAPFTGSS 300
Db 241 LLLLVIPIPAFWSLKTPLRLWKKIWAVSPERFPMPLKGCSDGDFKWKWGAPFTGSS 300
```

```
Qy 301 LELGWSPEVPSTLEVYSCHPSPAKRLQTLQEPALVESDGVKPSFWPTAQNSSG 360
Db 301 LELGWSPEVPSTLEVYSCHPSPAKRLQTLQEPALVESDGVKPSFWPTAQNSSG 360
Qy 361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDDAGLESPGLEPDL 420
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDDAGLESPGLEPDL 420
Qy 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480
Db 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480
Qy 481 PLAGLDMDTFDSGFVSGDCSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPOAS 538
Db 481 PLAGLDMDTFDSGFVSGDCSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPOAS 538
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## RESULT 6

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US-10-295-723-115
; Sequence 115, Application US/10295723
; Publication No. US20030125524A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030125524A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
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## US-10-295-723-115

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Query Match 100.0%; Score 2958; DB 14; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.3e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGWAAPLLLLLQGGWGPCDLVCYTDYLTQTVICILEMNLHPSTLTLTWQDQYEELKD 60
Db 1 MPRGWAAPLLLLLQGGWGPCDLVCYTDYLTQTVICILEMNLHPSTLTLTWQDQYEELKD 60
Qy 61 EATCSLHRSNAHNAHATYTCMDVHFHMADDIFSUNITDQSGNYSQCGSFLLAESIKP 120
Db 61 EATCSLHRSNAHNAHATYTCMDVHFHMADDIFSUNITDQSGNYSQCGSFLLAESIKP 120
Qy 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKQLQYELQYLRNRPDPAVSPRRKLISVDS 180
Db 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKQLQYELQYLRNRPDPAVSPRRKLISVDS 180
Qy 181 RSVSLLPLEFRKSSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGNPHLLL 240
Db 181 RSVSLLPLEFRKSSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGNPHLLL 240
Qy 240 RSVSLLPLEFRKSSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGNPHLLL 240
Db 240 RSVSLLPLEFRKSSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGNPHLLL 240
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Qy 241 LLLAVIVFIPAFWSLKTPLWRLWKIWA VSPSPERFFMPLYKCGSGDFKMWGAPFTGSS 300
Db 241 LLLAVIVFIPAFWSLKTPLWRLWKIWA VSPSPERFFMPLYKCGSGDFKMWGAPFTGSS 300
Qy 301 LELGWSPEVPSTLEVYSCHPSPAKRLQTLQEPALVESDGVKPSFWPTAQNSSG 360
Db 301 LELGWSPEVPSTLEVYSCHPSPAKRLQTLQEPALVESDGVKPSFWPTAQNSSG 360
Qy 361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDDAGLESPGLEPDL 420
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDDAGLESPGLEPDL 420
Qy 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480
Db 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480
Qy 481 PLAGLDMDTFDSGFVSGDCSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPOAS 538
Db 481 PLAGLDMDTFDSGFVSGDCSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPOAS 538

RESULT 7
US-10-282-622-16
; Sequence 16, Application US/10282622
; Publication No. US20030134390A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: No. US20030134390A1ak, Julia E.
; TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-282-622-16

Query Match 100.0%; Score 2958; DB 14; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.3e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGWAAPLLLLLQGGWGPCDLVCYTDYLTQTVICILEMNLHPSTLTLTWQDQYEELKD 60
Db 1 MPRGWAAPLLLLLQGGWGPCDLVCYTDYLTQTVICILEMNLHPSTLTLTWQDQYEELKD 60
Qy 61 EATCSLHRSNAHNAHATYTCMDVHFHMADDIFSUNITDQSGNYSQCGSFLLAESIKP 120
Db 61 EATCSLHRSNAHNAHATYTCMDVHFHMADDIFSUNITDQSGNYSQCGSFLLAESIKP 120
Qy 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKQLQYELQYLRNRPDPAVSPRRKLISVDS 180
Db 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKQLQYELQYLRNRPDPAVSPRRKLISVDS 180
Qy 181 RSVSLLPLEFRKSSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGNPHLLL 240
Db 181 RSVSLLPLEFRKSSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGNPHLLL 240
Qy 241 LLLAVIVFIPAFWSLKTPLWRLWKIWA VSPSPERFFMPLYKCGSGDFKMWGAPFTGSS 300
Db 241 LLLAVIVFIPAFWSLKTPLWRLWKIWA VSPSPERFFMPLYKCGSGDFKMWGAPFTGSS 300
Qy 301 LELGWSPEVPSTLEVYSCHPSPAKRLQTLQEPALVESDGVKPSFWPTAQNSSG 360
Db 301 LELGWSPEVPSTLEVYSCHPSPAKRLQTLQEPALVESDGVKPSFWPTAQNSSG 360
Qy 361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDDAGLESPGLEPDL 420
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDDAGLESPGLEPDL 420
```

Db 361 SAYSEERDRPYGLVSDITVTVLDAEGCTWPCSCDDGYPALDLADGLEPSPGLDPLLD 420  
QY 421 AGTTVLSGCCVAGSAGSLGGPLGSLDLRLKPPPLADGEDWAGGLPWGGRSPGVGSSEAGS 480  
Db 421 AGTTVLSGCCVAGSAGSLGGPLGSLDLRLKPPPLADGEDWAGGLPWGGRSPGVGSSEAGS 480  
QY 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVITPPPLSSPGQAS 538  
Db 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVITPPPLSSPGQAS 538

## RESULT 8

US-10-243-072-2  
; Sequence 2, Application US/10243072  
; Publication No. US2003014847A1  
; GENERAL INFORMATION:  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Conklin, Darrell C.  
; APPLICANT: No. US2003014847A1ak, Julia E.  
; APPLICANT: Hammond, Angela K.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL  
; FILE REFERENCE: 98-55C1  
; CURRENT APPLICATION NUMBER: US/10/243,072  
; PRIOR FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: 09/628,127  
; PRIOR FILING DATE: 2000-07-28  
; PRIOR APPLICATION NUMBER: US 60/100,896  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: US 60/123,546  
; PRIOR FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: US 60/142,574  
; PRIOR FILING DATE: 1999-07-06  
; PRIOR APPLICATION NUMBER: US 09/404,641  
; PRIOR FILING DATE: 1999-09-23  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-243-072-2

Query Match 100.0%; Score 2958; DB 14; Length 538;  
Best Local Similarity 100.0%; Pred. No. 2.3e-228;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MPRGWAAPLLLLLQGGWGPCDPLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60  
Db 1 MPRGWAAPLLLLLQGGWGPCDPLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60  
QY 61 EATCSLHRSNAHNAHTATYTCMDVHFHFMADDIFSVNITDQSGNYSQECGSLLAESIKP 120  
Db 61 EATCSLHRSNAHNAHTATYTCMDVHFHFMADDIFSVNITDQSGNYSQECGSLLAESIKP 120  
QY 121 APPFNVTTFSGQYNISWRSYEDPAFYMKGKQYELQYRNRPDPAWSPRKLISVDS 180  
Db 121 APPFNVTTFSGQYNISWRSYEDPAFYMKGKQYELQYRNRPDPAWSPRKLISVDS 180  
QY 121 APPFNVTTFSGQYNISWRSYEDPAFYMKGKQYELQYRNRPDPAWSPRKLISVDS 180  
Db 121 APPFNVTTFSGQYNISWRSYEDPAFYMKGKQYELQYRNRPDPAWSPRKLISVDS 180  
QY 181 RSVSLPLLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEBELKEGWNPHLLL 240  
Db 181 RSVSLPLLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEBELKEGWNPHLLL 240  
QY 241 LLLLVIPIPAFWSLKTPLWRLWKKIWAVSPERFFMPLKGCSDGDFKQWVGAFTGSS 300  
Db 241 LLLLVIPIPAFWSLKTPLWRLWKKIWAVSPERFFMPLKGCSDGDFKQWVGAFTGSS 300  
QY 301 LELGWSPEVSTLEVISCHPPRSAPAKRLQLTQELQPAELVESDGVKPKSPFWPTAQNCG 360  
Db 301 LELGWSPEVSTLEVISCHPPRSAPAKRLQLTQELQPAELVESDGVKPKSPFWPTAQNCG 360  
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGCTWPCSCDDGYPALDLADGLEPSPGLDPLLD 420  
Db 361 SAYSEERDRPYGLVSDITVTVLDAEGCTWPCSCDDGYPALDLADGLEPSPGLDPLLD 420

## RESULT 9

US-10-414-186-2  
; Sequence 2, Application US/10414186  
; Publication No. US20030175825A1  
; GENERAL INFORMATION:  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Conklin, Darrell C.  
; APPLICANT: No. US20030175825A1ak, Julia E.  
; APPLICANT: Hammond, Angela K.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL  
; FILE REFERENCE: 98-55  
; CURRENT APPLICATION NUMBER: US/10/414,186  
; PRIOR FILING DATE: 2003-04-14  
; PRIOR APPLICATION NUMBER: US/09/404,641  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-414-186-2

Query Match 100.0%; Score 2958; DB 14; Length 538;  
Best Local Similarity 100.0%; Pred. No. 2.3e-228;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MPRGWAAPLLLLLQGGWGPCDPLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60  
Db 1 MPRGWAAPLLLLLQGGWGPCDPLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60  
QY 61 EATCSLHRSNAHNAHTATYTCMDVHFHFMADDIFSVNITDQSGNYSQECGSLLAESIKP 120  
Db 61 EATCSLHRSNAHNAHTATYTCMDVHFHFMADDIFSVNITDQSGNYSQECGSLLAESIKP 120  
QY 121 APPFNVTTFSGQYNISWRSYEDPAFYMKGKQYELQYRNRPDPAWSPRKLISVDS 180  
Db 121 APPFNVTTFSGQYNISWRSYEDPAFYMKGKQYELQYRNRPDPAWSPRKLISVDS 180  
QY 181 RSVSLPLLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEBELKEGWNPHLLL 240  
Db 181 RSVSLPLLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEBELKEGWNPHLLL 240  
QY 241 LLLLVIPIPAFWSLKTPLWRLWKKIWAVSPERFFMPLKGCSDGDFKQWVGAFTGSS 300  
Db 241 LLLLVIPIPAFWSLKTPLWRLWKKIWAVSPERFFMPLKGCSDGDFKQWVGAFTGSS 300  
QY 301 LELGWSPEVSTLEVISCHPPRSAPAKRLQLTQELQPAELVESDGVKPKSPFWPTAQNCG 360  
Db 301 LELGWSPEVSTLEVISCHPPRSAPAKRLQLTQELQPAELVESDGVKPKSPFWPTAQNCG 360  
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGCTWPCSCDDGYPALDLADGLEPSPGLDPLLD 420  
Db 361 SAYSEERDRPYGLVSDITVTVLDAEGCTWPCSCDDGYPALDLADGLEPSPGLDPLLD 420  
QY 421 AGTTVLSGCCVAGSAGSLGGPLGSLDLRLKPPPLADGEDWAGGLPWGGRSPGVGSSEAGS 480

Db 421 AGTTVLSCGCVSAGSPGLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480  
Qy 481 PLAGLDMDTFDSGFGVSDSCSPVECDFTSPGDEGPPRSYLRQWVVIPTLSSPGPQAS 538  
Db 481 PLAGLDMDTFDSGFGVSDSCSPVECDFTSPGDEGPPRSYLRQWVVIPTLSSPGPQAS 538

RESULT 10  
US-10-456-780-6  
; Sequence 6, Application US/10456780  
; Publication No. US20040009150A1  
; GENERAL INFORMATION:  
; APPLICANT: Nelson, Andrew J.  
; APPLICANT: Hughes, Steven D.  
; APPLICANT: Holly, Richard D.  
; TITLE OF INVENTION: USE OF IL-21 IN CANCER AND  
; TITLE OF INVENTION: OTHER THERAPEUTIC APPLICATIONS  
; FILE REFERENCE: 03-08  
; CURRENT APPLICATION NUMBER: US/10/456,780  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: US 60/387,127  
; PRIOR FILING DATE: 2002-06-07  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-456-780-6

Query Match 100.0%; Score 2958; DB 15; Length 538;  
Best Local Similarity 100.0%; Pred. No. 2.3e-228;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGWAAPLLLLLLOGGCGCPDLVCYTDYLTQTVICILEMNNLHPSTLTLTWQDQYEELKD 60  
Db 1 MPRGWAAPLLLLLLOGGCGCPDLVCYTDYLTQTVICILEMNNLHPSTLTLTWQDQYEELKD 60  
Qy 61 EATCSLHRSAHNATHATYTCMDVDFHMADDIFSVNITDOSGNYSCGCSFLAESA1KP 120  
Db 61 EATCSLHRSAHNATHATYTCMDVDFHMADDIFSVNITDOSGNYSCGCSFLAESA1KP 120  
Qy 121 APPENVTVTFSGQYNISWRSYEDPAFYMLKGKQLQYELQYRNRGDPMVA5PRRKLISVDS 180  
Db 121 APPENVTVTFSGQYNISWRSYEDPAFYMLKGKQLQYELQYRNRGDPMVA5PRRKLISVDS 180  
Qy 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240  
Db 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240  
Qy 241 LLLLVIVIFAPFWSLKTHPLWRLWKIWA VSPERFPMPLKYGCSGDFKKWVGAPFTGSS 300  
Db 241 LLLLVIVIFAPFWSLKTHPLWRLWKIWA VSPERFPMPLKYGCSGDFKKWVGAPFTGSS 300  
Qy 301 LELGWPSPVSTLEVYSCHPSPRPAKRLQLTQELQEPALVESDGVKPSFWPTAQN5GG 360  
Db 301 LELGWPSPVSTLEVYSCHPSPRPAKRLQLTQELQEPALVESDGVKPSFWPTAQN5GG 360  
Qy 361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDLADGLESPGLEDPLLD 420  
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDLADGLESPGLEDPLLD 420  
Qy 421 AGTTVLSCGCVSAGSPGLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480  
Db 421 AGTTVLSCGCVSAGSPGLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480  
Qy 481 PLAGLDMDTFDSGFGVSDSCSPVECDFTSPGDEGPPRSYLRQWVVIPTLSSPGPQAS 538  
Db 481 PLAGLDMDTFDSGFGVSDSCSPVECDFTSPGDEGPPRSYLRQWVVIPTLSSPGPQAS 538

RESULT 11  
US-10-659-684-115

; Sequence 115, Application US/10659684  
; Publication No. US20040110932A1  
; GENERAL INFORMATION:  
; APPLICANT: Novak, Julia E.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Gross, Jane A.  
; APPLICANT: Johnston, Janet V.  
; APPLICANT: Nelson, Andrew J.  
; APPLICANT: Dillon, Stacey R.  
; APPLICANT: Hammond, Angela K.  
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND  
; FILE REFERENCE: 99-16  
; CURRENT APPLICATION NUMBER: US/10/659,684  
; CURRENT FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: US/09/522,217  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,547  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01  
; NUMBER OF SEQ ID NOS: 115  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 115  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-659-684-115

Query Match 100.0%; Score 2958; DB 16; Length 538;  
Best Local Similarity 100.0%; Pred. No. 2.3e-228;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGWAAPLLLLLLOGGCGCPDLVCYTDYLTQTVICILEMNNLHPSTLTLTWQDQYEELKD 60  
Db 1 MPRGWAAPLLLLLLOGGCGCPDLVCYTDYLTQTVICILEMNNLHPSTLTLTWQDQYEELKD 60  
Qy 61 EATCSLHRSAHNATHATYTCMDVDFHMADDIFSVNITDOSGNYSCGCSFLAESA1KP 120  
Db 61 EATCSLHRSAHNATHATYTCMDVDFHMADDIFSVNITDOSGNYSCGCSFLAESA1KP 120  
Qy 121 APPENVTVTFSGQYNISWRSYEDPAFYMLKGKQLQYELQYRNRGDPMVA5PRRKLISVDS 180  
Db 121 APPENVTVTFSGQYNISWRSYEDPAFYMLKGKQLQYELQYRNRGDPMVA5PRRKLISVDS 180  
Qy 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240  
Db 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240  
Qy 241 LLLLVIVIFAPFWSLKTHPLWRLWKIWA VSPERFPMPLKYGCSGDFKKWVGAPFTGSS 300  
Db 241 LLLLVIVIFAPFWSLKTHPLWRLWKIWA VSPERFPMPLKYGCSGDFKKWVGAPFTGSS 300  
Qy 301 LELGWPSPVSTLEVYSCHPSPRPAKRLQLTQELQEPALVESDGVKPSFWPTAQN5GG 360  
Db 301 LELGWPSPVSTLEVYSCHPSPRPAKRLQLTQELQEPALVESDGVKPSFWPTAQN5GG 360  
Qy 361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDLADGLESPGLEDPLLD 420  
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDLADGLESPGLEDPLLD 420  
Qy 421 AGTTVLSCGCVSAGSPGLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480  
Db 421 AGTTVLSCGCVSAGSPGLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480  
Qy 481 PLAGLDMDTFDSGFGVSDSCSPVECDFTSPGDEGPPRSYLRQWVVIPTLSSPGPQAS 538  
Db 481 PLAGLDMDTFDSGFGVSDSCSPVECDFTSPGDEGPPRSYLRQWVVIPTLSSPGPQAS 538



RESULT 12  
US-10-620-169-4  
; Sequence 4, Application US/10620169  
; Publication No. US20040136954A1  
; GENERAL INFORMATION:  
; APPLICANT: Grueby, Michael J  
; APPLICANT: Wurster, Andrea  
; APPLICANT: Young, Deborah  
; APPLICANT: Collins, Mary  
; APPLICANT: Whitters, Matthew  
; TITLE OF INVENTION: Methods and Compositions for Modulating T Helper (TH)  
; TITLE OF INVENTION: Cell Development and Function  
; FILE REFERENCE: 22058-585  
; CURRENT APPLICATION NUMBER: US/10/620,169  
; CURRENT FILING DATE: 2003-07-15  
; PRIOR APPLICATION NUMBER: 60/396,160  
; PRIOR FILING DATE: 2003-07-15  
; PRIOR APPLICATION NUMBER: 60/403,001  
; PRIOR FILING DATE: 2003-08-12  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-620-169-4

Query Match 100.0%; Score 2958; DB 16; Length 538;  
Best Local Similarity 100.0%; Pred. No. 2.3e-228;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MPRGAAPLLLLLQGGGCPDLVCYTDYLTQVTCILEMNNLHPSTLTLTWQDQYEELKD 60  
Db 1 MPRGAAPLLLLLQGGGCPDLVCYTDYLTQVTCILEMNNLHPSTLTLTWQDQYEELKD 60  
QY 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNSQCGSFLLAESIKP 120  
Db 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNSQCGSFLLAESIKP 120  
QY 121 APPFNVTTFSGQYNIWSRSDYEDPAFYMLKGKQLQYELQYRNRPDPAVSPRKLISVDS 180  
Db 121 APPFNVTTFSGQYNIWSRSDYEDPAFYMLKGKQLQYELQYRNRPDPAVSPRKLISVDS 180  
QY 181 RSVSLPLLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLLL 240  
Db 181 RSVSLPLLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLLL 240  
QY 241 LLLLVIVIPAFWSLKTPLRLWKKIWAVSPERFPMPLKGCSDGDFKKWVGAPFTGSS 300  
Db 241 LLLLVIVIPAFWSLKTPLRLWKKIWAVSPERFPMPLKGCSDGDFKKWVGAPFTGSS 300  
QY 301 LELGWSPEVSTLEVYSCHPPRSPAKRLQLTELOEPAELVESDGVKPKSPFWPTAQNSSG 360  
Db 301 LELGWSPEVSTLEVYSCHPPRSPAKRLQLTELOEPAELVESDGVKPKSPFWPTAQNSSG 360  
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLADGLESPGLDPLLD 420  
Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLADGLESPGLDPLLD 420  
QY 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGLPMGGRSPGVSSSEAGS 480  
Db 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGLPMGGRSPGVSSSEAGS 480  
QY 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538  
Db 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538

RESULT 13  
US-10-715-998-2  
; Sequence 2, Application US/10715998  
; Publication No. US20040204562A1

; GENERAL INFORMATION:  
; APPLICANT: Fresnell, Scott R.  
; APPLICANT: Conklin, Darrell C.  
; APPLICANT: Novak, Julia E.  
; APPLICANT: Hammond, Angela K.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11  
; FILE REFERENCE: 98-55  
; CURRENT APPLICATION NUMBER: US/10/715,998  
; CURRENT FILING DATE: 2003-11-18  
; PRIOR APPLICATION NUMBER: US/10/414,186  
; PRIOR FILING DATE: 2003-04-14  
; PRIOR APPLICATION NUMBER: US/09/404,641  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-715-998-2

Query Match 100.0%; Score 2958; DB 16; Length 538;  
Best Local Similarity 100.0%; Pred. No. 2.3e-228;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MPRGAAPLLLLLQGGGCPDLVCYTDYLTQVTCILEMNNLHPSTLTLTWQDQYEELKD 60  
Db 1 MPRGAAPLLLLLQGGGCPDLVCYTDYLTQVTCILEMNNLHPSTLTLTWQDQYEELKD 60  
QY 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNSQCGSFLLAESIKP 120  
Db 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNSQCGSFLLAESIKP 120  
QY 121 APPFNVTTFSGQYNIWSRSDYEDPAFYMLKGKQLQYELQYRNRPDPAVSPRKLISVDS 180  
Db 121 APPFNVTTFSGQYNIWSRSDYEDPAFYMLKGKQLQYELQYRNRPDPAVSPRKLISVDS 180  
QY 181 RSVSLPLLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLLL 240  
Db 181 RSVSLPLLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLLL 240  
QY 241 LLLLVIVIPAFWSLKTPLRLWKKIWAVSPERFPMPLKGCSDGDFKKWVGAPFTGSS 300  
Db 241 LLLLVIVIPAFWSLKTPLRLWKKIWAVSPERFPMPLKGCSDGDFKKWVGAPFTGSS 300  
QY 301 LELGWSPEVSTLEVYSCHPPRSPAKRLQLTELOEPAELVESDGVKPKSPFWPTAQNSSG 360  
Db 301 LELGWSPEVSTLEVYSCHPPRSPAKRLQLTELOEPAELVESDGVKPKSPFWPTAQNSSG 360  
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLADGLESPGLDPLLD 420  
Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLADGLESPGLDPLLD 420  
QY 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGLPMGGRSPGVSSSEAGS 480  
Db 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGLPMGGRSPGVSSSEAGS 480  
QY 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538  
Db 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538

RESULT 14  
US-10-872-087-2  
; Sequence 2, Application US/10872087  
; Publication No. US20040235743A1  
; GENERAL INFORMATION:

; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Novak, Julia E.  
; APPLICANT: West, James W.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Nelson, Andrew J.  
; APPLICANT: Hammond, Angela K.  
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS  
; FILE REFERENCE: 00-22D1  
; CURRENT APPLICATION NUMBER: US/10/872,087  
; CURRENT FILING DATE: 2004-04-18  
; PRIOR APPLICATION NUMBER: US 60/194,731  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/222,121  
; PRIOR FILING DATE: 2000-07-28  
; PRIOR APPLICATION NUMBER: US 09/825,561  
; PRIOR FILING DATE: 2001-04-03  
; NUMBER OF SEQ ID NOS: 86  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-872-087-2

Query Match 100.0%; Score 2958; DB 16; Length 538;  
Best Local Similarity 100.0%; Pred. No. 2.3e-228;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVTCILEMNLHPSTLTLTWQDQYEELKD 60  
Db 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVTCILEMNLHPSTLTLTWQDQYEELKD 60  
Qy 61 EATCSLHSAHNAHATYTTCHMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120  
Db 61 EATCSLHSAHNAHATYTTCHMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120  
Qy 121 APPFNVTTFSGQYNISWRSDYEDPAFVMLKGKQYELQYRNRGDPWAVSPRRKLIISVDS 180  
Db 121 APPFNVTTFSGQYNISWRSDYEDPAFVMLKGKQYELQYRNRGDPWAVSPRRKLIISVDS 180  
Qy 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLL 240  
Db 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLL 240  
Qy 241 LLLLVIVIFAPFWSLKTPLWRLWKIWA VSPERFPMPLKYGSGDPFKWVGAPFTGSS 300  
Db 241 LLLLVIVIFAPFWSLKTPLWRLWKIWA VSPERFPMPLKYGSGDPFKWVGAPFTGSS 300  
Qy 301 LELGPMSPVPSTLEVYCHPPRSPAKRLQLTQELQEPALVESDGVKPSFWPTAQNSGG 360  
Db 301 LELGPMSPVPSTLEVYCHPPRSPAKRLQLTQELQEPALVESDGVKPSFWPTAQNSGG 360  
Qy 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDLDAGLESPGLEDPILLD 420  
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDLDAGLESPGLEDPILLD 420  
Qy 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480  
Db 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480  
Qy 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPPLSSPGPQAS 538  
Db 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPPLSSPGPQAS 538

## RESULT 15

US-10-787-442-115  
; Sequence 115, Application US/10787442  
; Publication No. US2004026065A1  
; GENERAL INFORMATION:  
; APPLICANT: Novak, Julia E.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Foster, Donald C.

; APPLICANT: Holly, Richard D.  
; APPLICANT: Gross, Jane A.  
; APPLICANT: Johnston, Janet V.  
; APPLICANT: Nelson, Andrew J.  
; APPLICANT: Dillon, Stacey R.  
; APPLICANT: Hammond, Angela K.  
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND  
; FILE REFERENCE: 99-16  
; CURRENT APPLICATION NUMBER: US/10/787,442  
; CURRENT FILING DATE: 2004-02-26  
; PRIOR APPLICATION NUMBER: US/09/522,217  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: US 60/123,547  
; PRIOR FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: US 60/123,904  
; PRIOR FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: US 60/142,013  
; PRIOR FILING DATE: 1999-07-01  
; NUMBER OF SEQ ID NOS: 115  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 115  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-787-442-115

Query Match 100.0%; Score 2958; DB 16; Length 538;  
Best Local Similarity 100.0%; Pred. No. 2.3e-228;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVTCILEMNLHPSTLTLTWQDQYEELKD 60  
Db 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVTCILEMNLHPSTLTLTWQDQYEELKD 60  
Qy 61 EATCSLHSAHNAHATYTTCHMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120  
Db 61 EATCSLHSAHNAHATYTTCHMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120  
Qy 121 APPFNVTTFSGQYNISWRSDYEDPAFVMLKGKQYELQYRNRGDPWAVSPRRKLIISVDS 180  
Db 121 APPFNVTTFSGQYNISWRSDYEDPAFVMLKGKQYELQYRNRGDPWAVSPRRKLIISVDS 180  
Qy 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLL 240  
Db 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLL 240  
Qy 241 LLLLVIVIFAPFWSLKTPLWRLWKIWA VSPERFPMPLKYGSGDPFKWVGAPFTGSS 300  
Db 241 LLLLVIVIFAPFWSLKTPLWRLWKIWA VSPERFPMPLKYGSGDPFKWVGAPFTGSS 300  
Qy 301 LELGPMSPVPSTLEVYCHPPRSPAKRLQLTQELQEPALVESDGVKPSFWPTAQNSGG 360  
Db 301 LELGPMSPVPSTLEVYCHPPRSPAKRLQLTQELQEPALVESDGVKPSFWPTAQNSGG 360  
Qy 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDLDAGLESPGLEDPILLD 420  
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDLDAGLESPGLEDPILLD 420  
Qy 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480  
Db 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480  
Qy 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPPLSSPGPQAS 538  
Db 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPPLSSPGPQAS 538

Search completed: July 9, 2005, 12:00:42  
Job time : 165 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 9, 2005, 11:29:09 ; Search time 178 Seconds  
(without alignments)  
1547.745 Million cell updates/sec

Title: US-10-620-169-4

Perfect score: 2958

Sequence: 1 MPRGWAPLPLLLLLQGGWGC.....YLQWVWVPPPLSSFGPQAS 538

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2958	100.0	538	1 I21R_HUMAN	Q9bhe5 homo sapien
2	1735.5	58.7	529	1 I21R_MOUSE	Q9jthx3 mus musculus
3	872	29.5	268	2 Q6PEU8	Q6peu8 mus musculus
4	286	9.7	512	2 Q6UAP3	Q6uap3 tetraodon n
5	278	9.4	551	1 IL2B_HUMAN	P14784 homo sapien
6	250	8.5	890	2 Q9Z1L0	Q9z1l0 cavia porce
7	248	8.4	537	1 IL2B_RAT	P26896 rattus norv
8	247.5	8.4	539	1 IL2B_MOUSE	P16297 mus musculus
9	245.5	8.3	539	2 Q8R308	Q8r308 mus musculus
10	243.5	8.2	539	2 Q8CBU1	Q8cbu1 mus musculus
11	233	7.9	896	1 CYRB_MOUSE	P26955 mus musculus
12	231	7.8	896	2 Q8QZX9	Q8qzx9 mus musculus
13	226	7.6	529	2 Q5UAP7	Q5uap7 tetraodon n
14	221.5	7.5	468	1 IL9R_MOUSE	Q01114 mus musculus
15	221.5	7.5	631	2 Q6UAN4	Q6uan4 tetraodon n
16	218.5	7.4	419	2 Q6UAN6	Q6uan6 tetraodon n
17	218.5	7.4	878	1 IL3B_MOUSE	P26954 mus musculus
18	215	7.3	522	1 IL9R_HUMAN	Q01113 homo sapien
19	213.5	7.2	467	2 Q3Z216	Q3z216 rattus norv
20	213	7.2	508	1 EPOR_HUMAN	P19235 homo sapien
21	211.5	7.2	896	2 Q64146	Q64146 rattus sp.
22	211.5	7.2	896	2 Q78ZFS	Q78zfs rattus norv
23	210	7.1	469	2 Q8C2G1	Q8c2g1 mus musculus
24	206	7.0	889	2 Q6NSJ8	Q6nsj8 homo sapien
25	206	7.0	897	1 CYRB_HUMAN	P26954 mus musculus
26	204.5	6.9	903	2 Q6ICE0	Q6ice0 homo sapien
27	201	6.8	507	1 EPOR_MOUSE	P14753 mus musculus
28	199	6.7	509	1 EPOR_PIG	Q9myz9 sus scrofa
29	198	6.7	441	2 Q6UAP5	Q6uap5 tetraodon n
30	195	6.6	507	1 EPOR_RAT	Q07303 rattus norv
31	193.5	6.5	825	1 IL4R_HUMAN	P24394 homo sapien

RESULT 1  
121R\_HUMAN  
ID I21R\_HUMAN STANDARD; PRT; 538 AA.  
AC Q9BHE5; Q96HZ1; Q9HB91;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DE Interleukin 21 receptor precursor (IL-21R) (Novel interleukin receptor) (UNQ3121/PRO10273).  
GN Name=IL21R; Synonyms=NILR;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20531754; PubMed=11081504; DOI=10.1038/35040504;  
RA Parrish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C., Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S., Burkhead S., Heipel M., Brandt C., Kujiiper J.L., Kramer J., Conklin D., Presnell S.R., Berry J., Shlota F., Bort S., Hamby K., Mudri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T., Raymond F., Ching A., Yao L., Smith D., Webster P., Whitmore T., Maurer M., Kaushansky K., Holly R.D., Foster D.;  
RT "Interleukin 21 and its receptor are involved in NK cell expansion and regulation of lymphocyte function.";  
RL Nature 408:57-63(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20481926; PubMed=11016959; DOI=10.1073/pnas.200360997;  
RA Ozaki K., Kikly K., Michalovich D., Young P.R., Leonard W.J.;  
RT "Cloning of a type I cytokine receptor most related to the IL-2 receptor beta chain.";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:11439-11444(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";  
RL Genome Res. 13:2265-2270(2003).  
RN [4]  
RP SEQUENCE FROM N.A., AND VARIANTS CYS-191; ARG-318 AND SER-484.  
RA Rieder M.J., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;

Q6ua82 canis famil  
Q86325 sus scrofa  
P16382 mus musculu  
Q6uam6 tetraodon n  
Q9hc73 homo sapien  
Q8aup2 gallus gall  
Q63257 rattus norv  
Q6w224 equus cabal  
P40238 homo sapien  
P34902 mus musculu  
Q95n14 ovis aries  
Q91094 meleagris g  
Q95n13 ovis aries  
Q04594 gallus gall



05-JUL-2004 (Rel. 44, Last annotation update)

DE Interleukin 21 receptor precursor (IL-21R) (Novel interleukin  
DE receptor) (lymphocyte receptor beta) (IL-beta) (Novel cytokine  
DE receptor NR8).

GN Name=IL21R; Synonyms=Nilr;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RX MEDLINE=20531754; PubMed=11081504; DOI=10.1038/35040504;  
RA Parrish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C.,  
RA Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S.,  
RA Burkhead S., Heipel M., Brandt C., Kujipler J.L., Kramer J.,  
RA Conklin D., Presnell S.R., Berry J., Shioti F., Bort S., Hamby K.,  
RA Mudri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T.,  
RA Raymond F., Ching A., Yao L., Smith D., Webster P., Whitmore T.,  
RA Maurer M., Kaushansky K., Holly R.D., Foster D.;  
RT "Interleukin 21 and its receptor are involved in NK cell expansion and  
RT regulation of lymphocyte function.";  
RL Nature 408:57-63(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen, and Thymus;  
RX MEDLINE=20481926; PubMed=11016959; DOI=10.1073/pnas.200360997;  
RA Ozaki K., Kikly K., Michalovich D., Young P.R., Leonard W.J.;  
RT "Cloning of a type I cytokine receptor most related to the IL-2  
RT receptor beta chain.";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:11439-11444(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC Donaldson D.D., Whitters M.J., Fitz L., Unger M., Finnerty H.,  
RA Dagdigan C., Lowe L., Wood C.R., Young D.A., Collins M.;  
RT "Chromosome 16p12 encodes a biologically active IL-2Rb related  
RT receptor with lymphoid restricted expression.";  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Nomura H., Yaguchi N., Maeda M., Hasegawa M.;  
RT "A novel cytokine receptor NR8 is closely mapped to IL-4R:  
RT polymorphism in Balb/c mouse.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A/J, B10.S/DvTe, C57BL/6J, NOD/LtJ, and SJL/J; TISSUE=Spleen;  
RA Gao J., Teuscher C.;  
RT "Mus musculus interleukin 21 receptor gene Il21r mRNA.";  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: This is a receptor for interleukin-21.  
CC -!- SUBUNIT: Heterodimer with the common gamma chain. Associates with  
CC JAK1.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: Selectively expressed in lymphoid tissues.  
CC Most highly expressed in thymus and spleen.  
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein  
CC folding and thereby efficient intracellular transport and cell-  
CC surface receptor binding.  
CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or  
CC activation.  
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.  
CC Subfamily 4.  
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; AF254068; AAG29347.1; -  
DR EMBL; AF269134; AAG23420.1; -  
DR EMBL; AF279436; AAF86350.1; -  
DR EMBL; AB049137; BAB13736.1; -  
DR EMBL; AF477982; AAL82632.1; -  
DR EMBL; AF477983; AAL82633.1; -  
DR EMBL; AF477984; AAL82634.1; -  
DR EMBL; AF477985; AAL82635.1; -  
DR EMBL; AF477986; AAL82636.1; -  
DR MGI:1890475; IL21r.  
DR GO: 0004907; F:interleukin receptor activity; IDA.  
DR InterPro; IPR008957; FN\_III-like. Hemtrecepts\_F1.  
DR PROSITE; PS01355; HEMATOPO RECS\_F1; FALSE NEG.  
KW Glycoprotein; Polymorphism; Receptor; Signal; Transmembrane.  
FT SIGNAL 1 19  
FT CHAIN 20 529  
FT DOMAIN 20 237  
FT TRANSMEM 238 258  
FT DOMAIN 120 209  
FT DOMAIN 120 209  
FT SITE 214 218  
FT SITE 266 274  
FT DISULFID 25 35  
FT DISULFID 65 81  
FT CARBOHYD 73 73  
FT CARBOHYD 97 97  
FT CARBOHYD 104 104  
FT CARBOHYD 125 125  
FT CARBOHYD 182 182  
FT VARIANT 69 69  
FT VARIAT 200 200  
FT VARIAT V -> M (in strain BALB/c and strain SJL/  
FT J).  
SQ SEQUENCE 529 AA; 58354 MW; 8B41816B0D426581 CRC64;  
Query Match 58.7%; Score 1735.5; DB 1; Length 529;  
Best Local Similarity 62.7%; Pred. No. 1.1e-109;  
Matches 340; Conservative 49; Mismatches 136; Indels 17; Gaps 6;  
QY 1 MPRGWAAPLALLLGGGCPDLVCYTDYLTOTVTCILEMNLHPSTLTITWQDYEELKD 60  
DB 1 MERGVAALLLLHGAWSCLDLTCYTDYLTITTCVLETRSPNLSLTWQDYEELQD 60  
QY 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSNNITDQSGNYSQCGSFLLAESIKP 120  
DB 61 QETFCSLHRSAGNTHIWTTCMLSQFLSDEVFIVNTDQSGNNSQCGSFVLAESIKP 120  
QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYLKGLQYLOQRNRGDPWAVSPRRKLISVDS 180  
DB 121 APPLNVTVAFGRYDISWDSAYDBSPNVLKGLQYLOQRNLRDPYAVRPVKLISVDS 180  
QY 181 RSVSLLPLEFRKDSYELQVAGPMGSSYOGTSEWSDPVIQTQSELEKGNPHLL 240  
DB 181 RNVSLLPEEFKDSYQLQVRAAPQPGTSFGTSEWSDPVIQTQAGEAGNDPHMLL 240  
QY 241 LLLVIVIPAFWSLKTHTPLRWLKKIWA-VPSPERFFMPLYKGCSDGFKKVVWGAFTGS 299  
DB 241 LLAVLIIVL-VFMGLKHLPLRWLKKIWA-VPTTESFPQPLYRHSNGFKKVVWPTPTAS 299  
QY 300 SLELGPSPVPESTLEVYTSCHPPSPAKRQLQTELQEPALVESDGVKPKSPFW----PTAQ 356  
DB 300 SIELVPSQSTTTTSL-----HLSLYPAKEKKFPGLPGLEEQLECDGMSEPGHWCIPLAA 354  
QY 357 NSGSAVSEEDRDRPGLVSIIDTVTLDAEGCTWPCSCDDGYPALDLDAGLSPGLD 416  
DB 355 GQAVSAVSEEDRDRPGLVSIIDTVTVDAGELCVMPSCDDGYPAMNLDAGRESGNSD 414  
QY 417 PLLDAGTTVLSCGVSAGSGPLGGLSLDLRLKPLADGDWDAGGLPWGGRSPGVSES 476  
DB 415 LLLVTDPAFLSCGVSGLRLGSGPSGLDLRLRLUSPAKEGDWTDPTWRTGSPGGSES 474

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QY 477 EAGSPLAGLMDTDFSGVSCSPVCECDFTSPGDEGPRPSYLRQWVWVIPPPLSSPGPQ 536
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 475 EAGSP-PGLDMDTDFSGAGSDCGSPVET-----DEGPPRSYLEQWVVRTPPPVDSGAQ 527

QY 537 AS 538
:|
Db 528 SS 529

RESULT 3
Q6PEU8 PRELIMINARY; PRT; 268 AA.
AC Q6PEU8 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE IL1ir protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Matek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16989-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
RA Strausberg R. to the EMBL/GenBank/DBSJ databases.
RL Submitted (SEP-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC057861; AAH57861.1; --
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0004907; F:interleukin receptor activity; IDA.
DR InterPro; IPR008957; FN III-like.
SQ SEQUENCE 268 AA; 30A16 MW; B2EB0C31ACD6DA8 CRC64;

Query Match 29.5%; Score 872; DB 2; Length 268;
Best Local Similarity 69.6%; Pred. No. 2.3e-51;
Matches 158; Conservative 30; Mismatches 39; Indels 0; Gaps 0;

QY 1 MPRGWAALLLLLLGGGCPDLVCTDYLTQVICILEMNLHPSLTTLTWQDOYEELKD 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MPRGVAALLLLILHGANSCLDTCYTDYLTITICVLTSPNPSILSLTWQDEVEELQD 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 EATCSLHRSAHNATHATYTHMDFHFMADDIFSVNTDQSGNYSQCSFLAESTKP 120
:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 QETFCSLHRSGHNTTHIWTCHMRLSQFLSDEVFVNVTDQSGNNSQCSGFLAESTKP 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 APPENVVTFSGQYNISRSDYEDPAFYMLKGLQYELQYNRGDPWAVSPRKLISVDS 180
:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 APPLNVVTFASGRYDSDSDAYPEPSNVYLRGLQYELQYELQYNRDPYAVRPVTKLISVDS 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 181 RVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIFQTS 227
```

```
Db 181 RNVSLLPEEFHDKSSYLQVRAAPQPGTSPRGTWSESDPVIFQTA 227
|:||||| || |||||:||||| |||||:||||| |||||:||||| |||||:|||||
|:||||| || |||||:||||| |||||:||||| |||||:||||| |||||:|||||

RESULT 4
Q6UAP3 PRELIMINARY; PRT; 512 AA.
AC Q6UAP3 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Class I helical cytokine receptor member 13.
GN Name=CRFAL3;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP SEQUENCE FROM N.A.
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salancoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Bimont C., Skalli Z., Cattolico L., Poulain J., Berardinis Vd.,
RA Cruaud C., Duprat S., Brotier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.-N., Guigs R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quittier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Crolius H.R.;
RT "Analysis of the Tetraodon nigroviridis genome reveals the
RT proteokaryotype of bony vertebrates and its duplication in teleost
RT fish."
RL Nature 0:0-0(2004).
DR EMBL; AY374485; AAR25676.1; --
GO; GO:0004872; P:receptor activity; IEA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS0853; FN3; 1.
RX Receptor.
SQ SEQUENCE 512 AA; 57190 MW; E058418483A5DF0B CRC64;

Query Match 9.7%; Score 286; DB 2; Length 512;
Best Local Similarity 24.4%; Pred. No. 3.5e-11;
Matches 143; Conservative 76; Mismatches 203; Indels 164; Gaps 29;

QY 10 LLLLLGGGCPDLV-----CYTDYLTQVIC-ILEMNLHPSLTTLTWQDOYEELKDEA 62
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 14 LLLFPVQ----CAAVSRNCNTCTDYNVSLNCSCAEAVQTRSVFLHVKCSDEGIDVED-- 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 63 TSCSLHRSAHNATHATYTHMDFHFM-----DDIFSVN-----ITDQSGN--YSQ 107
:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 68 -----SCEVKPFQSCVMSPESEDLVSVTMCARATDGDGAPIDSS 110
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 108 ECGSFLAESTKIPAPPNVTVT-FSGQYNISW-RSDYEDPAFYMLKGLQYELQYNRGD 165
:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 111 ESPSWALCDVVKVPPSAVRVNTEDSYNTVTHVNLQDCLTYVVR-----VREANR-- 162
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 166 PWAVSPRKLISVDSRSVSLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPV-IFQ 224
:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 163 -WSKEPVYSL-SSDSKHLQIISPELLQPRVGLVDVKAMCPGKLYEGPWSSESSAEIRP 220
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 225 TQSEBELKEGNPHLL-----LLLLLVIFIPAFWMSLXTHPLRWLWKKIWAVPSPERFMP 279
:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 221 AATSDIAMS--HLFYITPSVLTVVVVSVLSVLSYLIKNH-----QIPKEHFFAP 268
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 280 LYKCSGDFKWKVGAFF-----TGSSL-----ELGPWSPEVPSTLEVYSCHPSPSPA 326
:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 269 LYHNYGDFKEWVNFVFEKCDYLMIGSOVMKNQSDLLQWNSEKSESTESKMNKHGHHF 328
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 327 KRLQLTELOPAPLVSDDGVKPSFPTAQNCGGSAYSEERDRPYGLVSDITVTVDAB- 385  
 DB 329 PKLQAO--AHPLLGSDWG-----SQSRGLA-----GFSIHTVTLSEEE 368  
 QY 386 -----GPTWPCSCEDDGYPALDLDAGLSPSPGLDPLLDAGTTVLSCGCVSAGSP 436  
 DB 369 FEEGTSQSSACVLRSDQRESEFVFDWKEQAUGLEE-----AASGLP 414  
 QY 437 GLGGPIGLSLDRKPLPADGEDWAGLPGMGSPGVS-----ESRAGSPLAGLMD 488  
 DB 415 -----PVLQQRASRSSGEGDDVPLPHQFFRAERVSLDLSLALNDQSDGYP--HVDLD 465  
 QY 489 TPDGFGVSGDCSPVCDFTSPGEGPP-----RSLQWVV 525  
 DB 466 TIDSGF--GEYNSP-----GASPGADQTSLSHEHNLHLSNYVQMWV 505

RESULT 5  
 IL2B HUMAN STANDARD; PRT; 551 AA.  
 AC P14784;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Interleukin-2 receptor beta chain precursor (IL-2 receptor) (P70-75)  
 DE (High affinity IL-2 receptor beta subunit) (CD122 antigen).  
 GN Names: IL2RB;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89242117; PubMed=2785715;  
 RA Hatakeyama M., Tsudo M., Minamoto S., Kono T., Doi T., Miyata T.,  
 Miyasaka M., Taniguchi T.;  
 R# "Interleukin-2 receptor beta chain gene: generation of three receptor  
 RT forms by cloned human alpha and beta chain cDNA's";  
 RT Science 244:551-556(1989).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RA Rieder M.J., Amel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,  
 Rajkumar N., Roth E.J., Yi Q., Nickerson D.A.;  
 RT "SeattLESNP: NHLBI HL6682 program for genomic applications, UW-  
 RT FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;  
 RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,  
 Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,  
 Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,  
 Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,  
 Burrill W.D., Burton J., Carter C., Carter N.P., Chen Y., Clark G.,  
 Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,  
 Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,  
 Dhani P.D., Dockree C., Doddsworth S.J., Durbin R.M., Ellington A.G.,  
 Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,  
 Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,  
 Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,  
 Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,  
 Laird G.K., Langford C.F., Levensha M.A., Lloyd C., Lloyd D.M.,  
 McLaren I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,  
 McEllyn J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,  
 Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,  
 Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,  
 Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,  
 Soderlund C., Spragon L., Steward C.A., Sulston J., Swann R.M.,  
 Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,  
 Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,  
 Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,  
 Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,

RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,  
 Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,  
 Dorman A., Fang F., Fu Y., Hua A., Kanton S., Lai H., Lao H.I.,  
 Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,  
 Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,  
 Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,  
 Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,  
 Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,  
 Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,  
 Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,  
 Rofe I., Bedell J.A., Wamsley A., Wohlmann P., Pepin K., Nelson J.,  
 Korfei P., Hillier L.W., Mardis E., Waterston R.,  
 Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,  
 Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,  
 Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,  
 Peyraud M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,  
 O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,  
 Khan A.S., Lane L., Tilahun Y., Wright H.;  
 RT "The DNA sequence of human chromosome 22.";  
 RL Nature 402:489-495(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Frange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Faye J., Helton E., Kettner M., Maman A., Rodriguez S., Sanchez A.,  
 Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M.,  
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [5]  
 RP 3D-STRUCTURE MODELING OF 31-230.  
 RX MEDLINE=95111955; PubMed=7529123;  
 RA Bamorough P., Hedgecock C.J., Richards W.G.;  
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular  
 modelling.";  
 RL Structure 2:839-851(1994).  
 CC -!- FUNCTION: Receptor for interleukin 2. This beta subunit is  
 involved in receptor mediated endocytosis and transduces the  
 mitogenic signals of IL2.  
 CC -!- SUBUNIT: Noncovalent dimer of an alpha and a beta chains. IL2R  
 exists in 3 different forms: a high affinity dimer, an  
 intermediate affinity monomer (beta chain), and a low affinity  
 monomer (alpha chain). The high and intermediate affinity forms  
 also associate with a gamma chain.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein  
 folding and thereby efficient intracellular transport and cell-  
 surface receptor binding.  
 CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or  
 activation.  
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.  
 CC -!- SIMILARITY: Subfamily 4.  
 CC -!- SIMILARITY: Contains 1 fibronectin type III domain.  
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD122 entry;  
 WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd122.htm".  
 CC -----  
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DR EMBL; M26062; AAA59143.1; --  
DR EMBL; AF517934; AAM54040.1; --  
DR EMBL; AL022314; -- NOT\_ANNOTATED\_CDS.  
DR EMBL; BC025691; AAH25691.1; --

DR FIR; A30342; A30342.  
DR PDB; 1ILM; Model; B=31-230.  
DR PDB; 1ILN; Model; B=31-230.  
DR Genew; HGNC:6009; IL2RB.

DR H-invDB; HIX0016437; --  
DR MW; 146710; --

DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
DR GO; GO:0004911; F:interleukin-2 receptor activity; TAS.  
DR GO; GO:0006461; P:protein complex assembly; TAS.  
DR GO; GO:0007165; P:signal transduction; TAS.

DR InterPro; IPR002296; Cytokn\_recept\_B/G.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR003531; HemtreceptS\_F1.  
DR PROSITE; PS01353; FN3; 1.

DR PROSITE; PS01355; HEMATOPO\_REC\_S\_F1; 1.  
KW 3D-structure; Glycoprotein; Receptor; Signal; Transmembrane.

FT SIGNAL 1 26  
FT CHAIN 27 551 Interleukin-2 receptor beta chain.  
FT DOMAIN 27 240 Extracellular (Potential).  
FT TRANSMEM 241 265 Potential.

FT DOMAIN 266 551 Cytoplasmic (Potential).  
FT DOMAIN 131 229 Fibronectin type-III.  
FT SITE 220 224 WSXWS motif.  
FT SITE 278 286 Box 1 motif.

FT SITE 36 46 By similarity.  
FT DISULFID 74 86 By similarity.  
FT CARBOHYD 29 29 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 43 43 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 71 71 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 149 149 N-linked (GlcNAc...) (Potential).  
FT STRAND 35 37  
FT STRAND 45 47  
FT STRAND 52 52  
FT STRAND 56 56  
FT STRAND 60 64  
FT STRAND 68 70

FT STRAND 72 73  
FT TURN 80 82  
FT STRAND 85 86  
FT TURN 90 92  
FT TURN 93 95  
FT HELIX 99 104  
FT STRAND 112 116  
FT STRAND 132 133  
FT STRAND 139 142  
FT STRAND 149 150  
FT STRAND 159 160  
FT TURN 163 169  
FT STRAND 178 180  
FT STRAND 185 186  
FT TURN 200 201  
FT STRAND 205 206  
FT STRAND 208 210  
FT TURN 215 216  
FT STRAND 221 221  
FT STRAND 227 228

SQ SEQUENCE 551 AA; 61117 MW; 1A76FA1936BB7EE6 CRC64;  
Query Match 9.4%; Score 278; DB 1; Length 551;  
Best Local Similarity 26.0%; Pred. No. 1.4e-10;  
Matches 137; Conservative 75; Mismatches 199; Indels 116; Gaps 31;

QY 5 WAAPLLILL--LQGGW-----GCPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYE 56

Db 8 WRLPLLILLPLATSWASAAVNGTQFTCFYNSRANISCV---WS-----QDG 52  
QY 57 ELKDEATSCSIH---RSAINAT-----HATVTCM-----DVHFMADDISVMTD 100  
Db 53 ALQD--TSCQVHAMPDRRRNQTCELLPVSQASMACNLILGAPDSQKLTVDIVTLRVLC 110  
QY 101 QSGNYSQECG--SFLLAESIKPAPPFNVTVF--SQQYNISWRSYEDPDPAFMYLKGLO 156  
Db 111 REGYRWVMAIQDKPFENLRMAPISLQVHVHETHRCNISWEI---SQASHYFERHLEF 167  
QY 157 ELQYNRGDPMAVSPRKLISVDSRSVSLPLLEPRKDSSELQVRAQMPGSSVQGTWSE 216  
Db 168 EARTLSPGHTWEAP--LLTLKQKQEWICLETITPDQYEFQVRVKPLQGEF--TTWSP 222  
QY 217 WSDPVIFQTQSEELKEG---WNPHLLLLLLLVIFAFWSL-----KTHPLRWLW-KKI 268  
Db 223 WSQPLAPRTKPAALGKDTIPWLGHLVLGLSGAFIILVLLINCRNTGP-----WLKKVL 278  
QY 269 A--VPSPERFFMPLYKGCSDGDKKVGAPFTGSSLELGPWSPPEVPSTLEVYSCHPPRSPA 326  
Db 279 KCNTPDPSKFFSLSSEHGQVQKWLSSFPSSSFSGGLAPEI-SPLEV-----L 328  
QY 327 KRLQTELOQPAELVESDGVKPSFWPTAONGSGSAYSEERDRPYGLVSDITVTVLDAEG 386  
Db 329 ERDKVTQL-----LLQDKVPEPA-----SLSSNHSLSCTFNQGYFFFLPDALEIEA-- 377  
QY 387 PC-----TPWCSCEDD-----GYPALDDAGLESPGLEPDLDDAGTTVLSCGCVSAGSP 436  
Db 378 -CQVFTYDPSYSEEDPDGAGAPTGSPOPLQPLSG-ED--DAYCTFSRDDLLLFSP 432  
QY 437 G-LGGP-----LGSLLDRKLPPLAD--GEDWAGGLPWGGRSPG 471  
Db 433 SLLGGPSPPTAPGSGAGEERWPPSLQERVRDW-DPQPLGPPPTG 478

RESULT 6

Q9Z1A0  
ID Q9Z1A0 PRELIMINARY; PRT; 890 AA.  
AC Q9Z1A0;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Interleukin-5 receptor beta chain.  
GN Name=IL5;  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Logsdon N.J., Graham A., Scott C.W.;  
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U94688; AAC77520.1; --  
DR HSSP; P32927; 1GH7.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004907; F:interleukin receptor activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0019221; P:cytokine and chemokine mediated signaling p...; IEA.  
DR InterPro; IPR002996; Cytokn\_recept\_B/G.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR InterPro; IPR003531; HemtreceptS\_F1.  
DR InterPro; IPR011365; IL3recept\_beta\_c.  
DR Pfam; PF00041; fn3; 3.  
DR PIRSF; PIRSF001956; IL3R\_beta\_c; 1.  
DR SMART; SM00060; FN3; 3.  
DR PROSITE; PS00853; FN3; 2.  
DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; UNKNOWN\_1.  
DR PROSITE; PS01355; HEMATOPO\_REC\_S\_F1; UNKNOWN\_1.  
KW Receptor.  
SQ SEQUENCE 890 AA; 96578 MW; D43FB1CA88525536 CRC64;

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Query Match      8.5%; Score 250; DB 2; Length 890;
Best Local Similarity 22.7%; Pred. No. 2e-08;
Matches 150; Conservative 73; Mismatches 217; Indels 220; Gaps 36;

QY 2 PRGWAAPLALLLQGGGCP-DLVCVTDYLTQVTCILEMNLHPSTLTLTW-----51
DB 229 PSQMSPEVSSQPGDQAPQNLQCVDFGAHLSCSWEVSQVTSVSGLYFRSLDAG 288
QY 52 -----QDQYELKDEAT--SCSLHRSAAHNAHATATYCHMDVDFHFMADDFISVNTDQSG- 103
DB 289 EQECPOVQKEELHDIYTRHSCQI-RVSNRPHSQYI-----VTVRPNRGE 332
QY 104 NYSQECGSLLEASIKPAPFPNVTTFSCQYNISWRSDYEDPAFYMKGKLYEQLQYRNR 163
DB 333 KPIRSANHIQMA-----APLNVTKD-GDYSRLRWVTE-----KMYSHIENTFEIQRTA 382
QY 164 GDPWAVSPRRKLISVDSRSVSLPLLEFRKDSYELQVRAGPMPGSSYQCTWSEWSDPVIF 223
DB 383 GDRWENSKTETL--KNAHNPPLPLE--PATYILARVRKPSPGGAYNGIWSNEEQRW 438
QY 224 QTSQELKEGWN-PHLLLLLVIVIP-----AFWSLKHPLRLMKKIMAVSPSPRFF 277
DB 439 TTD-----WALPTWLVALLVLTALLLALRFGGLVGYRLNRKWE--KIPNPSKSH 489
QY 278 M-----PLYKCGSGDKKWWG-APTGSLSLELGPWSPVPSTL 314
DB 490 LFKNGSAGLRLPDRMAFASRAPSNGVMGRFLIEGVCPADSRDSEVSLTTEDPTV 549
QY 315 EYVSHPPSPKRIQLTQLQPAELVESDGVKPSFMTAQNQSGSAYSEBERDPYGLV 374
DB 550 -----CDPPEPSTPAASDLTQEPSPVQGPVP-----QDQFG---585
QY 375 SIDTVTLDAEGFCTWP-----CSCBDDG-----YPALDLID 405
DB 586 -----DQLATDFNGPYLGPSPHSHSLDLAGQQGKPELPGSLVCLPPGGAQLVLAQAT 643
QY 406 AGLESPGLEDLIDAGTTVLSG--GCVSAGSFG--GGPLGSLDLRLKPLADGEDWA 460
DB 644 GOAQAPAP-----ECLSGPVTOGSPYLEAGGPP-----APPASDPGSA 682
QY 461 GGLPWGGRSPGG--VSSEAGSPLAGLMDMTDFDSGFV-----GSDCSS-----P 502
DB 683 QG-----PGDGPSPVILPTNSGGP-----EHPVVASGYVTADLAULTSTEASSVSLAPPP 735
QY 503 VECDFTS-----PGDEGP-PRSVLROWWVTP-----PLSSPG-PQ 536
DB 736 DLCPGLSDEAPAAPTPGKPRFGYVELPASMGFLPKSFLGGFV--PPAPSSVLSFGTFQ 793

RESULT 7
ID IL2B RAT
AC P26896;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-2 receptor beta chain precursor (IL-2 receptor) (P70-75)
DE (High affinity IL-2 receptor beta subunit) (CD122).
GN Name=IL2rb;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91364784; PubMed=1889461;
RA Page T.H., Dailman M.J.;
RT "Molecular cloning of cDNAs for the rat interleukin 2 receptor alpha
RT and beta chain genes; differentially regulated gene activity in
RT response to mitogenic stimulation";
RL Eur. J. Immunol. 21:2133-2138(1991).
CC -!- FUNCTION: Receptor for interleukin 2. This beta subunit is
```

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involved in receptor mediated endocytosis and transduces the
mitogenic signals of IL2.
-!- SUBUNIT: Noncovalent dimer of an alpha and a beta chains. IL2R
exists in 3 different forms: a high affinity dimer, an
intermediate affinity monomer (beta chain), and a low affinity
monomer (alpha chain). The high and intermediate affinity forms
also associate with a gamma chain.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
folding and thereby efficient intracellular transport and cell-
surface receptor binding.
-!- DOMAIN: The box 1 motif is required for JAK interaction and/or
activation.
-!- SIMILARITY: Belongs to the type I cytokine family of receptors.
Subfamily 4.
-!- SIMILARITY: Contains 1 fibronectin type III domain.
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or send an email to license@isb-sib.ch).
CC
CC EMBL; M55050; AAA1429.1; -.
CC DR HSP; P14784; IILM.
CC DR RGD; 2896; IL2rb.
CC DR InterPro; IPR002996; Cytokn_recept_B/G.
CC DR InterPro; IPR008957; FN_III-like_F1.
CC DR InterPro; IPR003531; Hemptrecept_F1.
CC DR PROSITE; PS00853; FN3; 1.
CC DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
CC KW Glycoprotein; Receptor; Signal; Transmembrane.
CC FT SIGNAL 1 26
CC FT CHAIN 27 537
CC FT DOMAIN 27 239
CC FT TRANSMEM 240 537
CC FT DOMAIN 268 537
CC FT DOMAIN 132 230
CC FT SITE 221 225
CC FT SITE 280 288
CC FT DISULFID 36 46
CC FT DISULFID 74 86
CC FT CARBOHYD 43 43
CC FT CARBOHYD 55 55
CC FT CARBOHYD 71 71
CC FT CARBOHYD 150 150
CC SQ SEQUENCE 537 AA; 60657 MW; 9C744A24F3361968 CRC64;

Query Match      8.4%; Score 248; DB 1; Length 537;
Best Local Similarity 23.6%; Pred. No. 1.4e-08;
Matches 148; Conservative 70; Mismatches 178; Indels 232; Gaps 33;

QY 5 WAAPL--LLLLLQGGW-----GCPDLVCYTDYLTQVTCILEMNLHPSTLTWTQDQVE 56
DB 8 WRLPLYILLLLATTWVSAAVNDCSHLCKFYNSRANVSC---MWS-----49
QY 57 ELKDEA---TSCSLHRSAAH---NAT-----HATYTCM-----DVDFHFMADDFSV 96
DB 50 --PBEALNVTSCHHAKSDMRHWNKTCELTPVQASMAKNLILGPLDQSLTSVLLLSL 107
QY 97 NIT--DOSGNYSQBCSGFLAESIKPAPFPNVTTF--SGQYNISWR-----SDYEDPAFY 148
DB 108 SVVCWEKGRVRVKTCTFHPFDNLRLIAPHSLQVLHIETRCNISWEVSQVSHYVNP---164
QY 149 MLKGLQYELQYRNGDPAVSPRRKLISVDSRSVSLPLLEFRK-----DSSVEL 198
DB 165 ---YLEPE-----ARRLLDRSWEDASVSLKQKQWIFLETLTPTDTSYEL 207
QY 199 QVRAGPMPGSSYQCTWSEWSDPVIFQOSEELKEGNPHLLLLLVIVFPAFWS-----254
DB 208 QVRVIAORGKT--RTWSPWSQPMAPFTRPADPKEIFPLWLRCLLLVLGFCFFGLSCVCV 265
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RX MEDLINE=90319131; PubMed=1695379;
RA Gorman D.M., Itoh N., Kitamura T., Schreurs J., Yonehara S.,
RA Yahara I., Arai K., Miyajima A.;
RT "Cloning and expression of a gene encoding an interleukin 3 receptor-
RT like protein: identification of another member of the cytokine
RT receptor gene family.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5459-5463(1990).
CC -!- FUNCTION: High affinity receptor for interleukin-3, interleukin-5
CC and granulocyte-macrophage colony-stimulating factor.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain. The beta chain
CC is common to the IL3, IL5 and GM-CSF receptors.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding.
CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 4.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M34397; AAA37204.1; -.
DR PIR; A35782; A35782.
DR HSSP; P32927; 1GH7.
DR MGD; MGI:1339759; Csf2rb1.
DR InterPro; IPR002996; Cytokn_recept_B/G.
DR InterPro; IPR000282; Cytok_receptor_2.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003531; Hemtrecepts_F1.
DR PIRSF; PIRSF01956; IL3R_beta_c; 1.
DR PROSITE; PS01355; HEMATOPO_REC_SF_1; 1.
DR KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 22 Potential.
FT CHAIN 23 896 Cytokine receptor common beta chain.
FT DOMAIN 23 441 Extracellular (Potential).
FT TRANSMEM 442 463 Potential.
FT DOMAIN 464 896 Cytoplasmic (Potential).
FT DOMAIN 132 241 Fibronectin type-III 1.
FT DOMAIN 343 440 Fibronectin type-III 2.
FT SITE 428 432 WSXWS motif.
FT SITE 477 485 Box 1 motif.
FT DISULFID 39 49 By similarity.
FT DISULFID 77 99 By similarity.
FT DISULFID 88 94 By similarity.
FT DISULFID 253 263 By similarity.
FT DISULFID 292 310 By similarity.
FT CARBOHYD 62 62 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 141 141 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 350 350 N-linked (GLCNAC...) (Potential).
SQ SEQUENCE 896 AA; 99111 MW; 8CE16EDFDC07A999 CRC64;

Query Match 7.9%; Score 233; DB 1; Length 896;
Best Local Similarity 20.4%; Pred. No. 2.8e-07;
Matches 113; Conservative 86; Mismatches 220; Indels 134; Gaps 23;

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D 250 NLQCFDGIQLSHCSWEVWTTQTSVSGLYFRSPVA-----PEKCFPVKEP 299
QY 71 ANHATHATYTCMDVHFHMADDFSVNITDQSGYQSCGSFLLA-ESIKAPP-FNVTV 128
D 300 PGASVYTRYHCSLPLPEPSAHSQVTVSVK-----HLEQGKFINSYNHIOEPTLNLTK 353
QY 129 TFSQYNISWSDYEDPAFYMLKGLQYELQYRNGDPWVSPRKLISVDSRVSLLPL 188
D 129 TFSQYNISWSDYEDPAFYMLKGLQYELQYRNGDPWVSPRKLISVDSRVSLLPL 188

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Db 354 N-RDSYSLHWETQKAYSFI-----EHTQVQVKKKSDSWEDSKTENLDRAHMSDLS----- 404
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D 405 QLEPDTSYCARVRVKPI--SNYDGIWSKWSEYTWKT-DWVMTPLWIVLILVFLILTL 461
QY 249 IPAFWSLTKTHPLRWLWKIWIWVSPERFPMFLYKCGSDGFKWVGAPFTGSSLELGPWSP 308
D 462 ILRFGCVSVYTRYKWKKE--KIPNPSKLL-----FQDGGKGLWP----- 499
QY 309 EVPSTLEYVCHPP--RSPAKRLQLTQEPALVELVESDGVKPKSPWPTAQNSSGSAVSEE 366
D 500 --PGSMAAFATNPAALQGPQSRLL-LAEQQ-----GESYAHLL 532
QY 367 RDRPYGLVSDITVTVL--DAEGPCTWPCSD--DGYPALDLDAGLESPSGLEDPLLDAG 422
D 533 EDNVPSPLETDENIIRVPPSPDTPPAASESTEQLPNVQVEGTPNRPKRQLPSFD-- 590
QY 423 TTVLSGCGVSAGSPGLGSP-----LGSLLDLRLKPPLADGE---DWAGGLPWGGRSPGG--- 472
D 591 -----FNGPYLGPQSHSLPDLQQLGSPQVGGSLKPLPAGSLPYMCLAFGGVQ 640
QY 473 -----VSESEAGSPLAGLMDTDFDSGFVGDSCSSPVCEDTSPDGGPPRSYLRQWV 525
D 641 LVPLSQWVGQQANDVQCGSSLETSGSPSVPEKPNPPVELSMERQEARDNP----- 691
QY 526 IPPPLSSPGQAS 538
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AC Q8QZX9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Interleukin 3 receptor-like protein.
GN Name=Csf2rb1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21363810; PubMed=11471062;
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
RT "High-throughput sequence identification of gene coding variants
RT within alcohol-related QTLs.";
RL Mamm. Genome 12:657-663(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ILS, and ISS;
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF483496; AAL90770.1; -.
DR EMBL; AF483497; AAL90771.1; -.
DR HSSP; P32927; 1GH7.
DR MGD; MGI:1339759; Csf2rb1.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR002996; Cytok_recept_B/G.
DR InterPro; IPR000282; Cytok_receptor_2.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003531; Hemtrecepts_F1.
DR InterPro; IPR011365; IL3recept_beta_c.
DR Pfam; PF00041; fn3; 2.
DR PIRSF; PIRSF001956; IL3R_beta_c; 1.

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Db	334	-----PQARQNGVSTSSAGSES-----SIW	353
Qy	377	DTVTVLDAEGPCTWPCSC-----EDDGYPALDLDAGLEPSPGLEDPLLDAGTTVLSCGCV	431
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Qy	432	S-AGSPGLGGPLGSLDLRLPLADGEDWAGGLPWGGRSPGVSESEAGSPLAGLMDMTF	490
Db	397	ELEGQPSAYLP-----QEDWA---PLGSARP-PPPPSDSGS-----	428
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DT	05-JUN-2004	(TREMBlrel. 27, Created)	
DT	05-JUN-2004	(TREMBlrel. 27, Last sequence update)	
DT	05-JUN-2004	(TREMBlrel. 27, Last annotation update)	
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GN	Name=CRFA22;		
OS	Tetraodon nigroviridis	(Green puffer).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;		
OC	Tetraodontoidea; Tetraodontidae; Tetraodon.		
OX	NCBI_TaxID=99883;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Jallion O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,		
RA	Mauceli E., Bouteau L., Fischer C., Ozouf-Costaz C., Bernot A.,		
RA	Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,		
RA	Dasilva C., Salanoubat M., Levy M., Boudet N., Castellan S.,		
RA	Antouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,		
RA	Bimont C., Skalli Z., Catalico L., Poulain J., Berardinis Vd.,		
RA	Cruad C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,		
RA	Parra G., Lardier S., Chappelle C., McKernan K.J., McEwan P., Bosak S.,		
RA	Kellis M., Wolff J.-N., Guigs R., Zody M.C., Mesirov J.,		
RA	Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,		
RA	Laudet V., Schachter V., Quittier F., Saurin W., Scarpelli C.,		
RA	Winkler P., Lander E.S., Weissenbach J., Crolius H.R.;		
RT	"Analysis of the Tetraodon nigroviridis genome reveals the		
RT	protocaryotype of bony vertebrates and its duplication in teleost		
RT	fish."		
RL	Nature 0:0-0(2004).		
RL	ENBL; AY374494; AAR25685.1; -.		
DR	GO; GO:0004872; F:receptor activity; IEA:		
DR	InterPro; IPR003961; FN.III.		
DR	InterPro; IPR008957; FN.III-like.		
KW	PROSITE; PS00853; FN3; 1.		
KW	Receptor.		
SEQ	SEQUENCE 631 AA; 71679 MW; A8922F3F748CD148 CRC64;		
Query Match 7.5%; Score 221.5; DB 2; Length 631;			
Best Local Similarity 25.7%; Pred. No. 1.1e-06;			
Matches 125; Conservative 57; Mismatches 166; Indels 139; Gaps 32			
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QY 111 SFLLA--ESIKPAPFNVTTFSGQYNISWRSD-----YEDPAFYMLKGLQYELQYENR 163  
Db 321 TPVLAAYKSIRTSPPSHL-----SG-----GWRNRKLCWKWETP-LPILFAHLQYEVFYQIR 371  
QY 164 G-DPMAVSPRRKLISVDSRSVSL---LPLEFRKOSSEYELQVRAGFMPGSGSYQGTWSEWS 219  
Db 372 GTDANTI-----LSIQSAETSTCVQLPLGIH-----YRAKIRAKP-DGITYSGDMSDSD 420  
QY 220 PVIFOTQSEELKEGNPHLL---LLLLVIVFIPAFWSLKTPLWRLWKKIW-AVPSPER 275  
Db 421 VITGTPADK-----STELLICIPICMLVIAVITISLPKTFSKLKY--FWPPVPNBDK 473  
QY 276 FMPLYKCSGDFKXWVGAPFTGSSLELGPNSPEVP-----STLEVYSCHPPRSAPKR 328  
Db 474 VLQGYLTING--QRW-----NPMWTTKPCLEDIAAGFLEVMSDEAVVSEKR 519  
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Db 624 LYTNLPC 630

Search completed: July 9, 2005, 11:47:03  
Job time : 181 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 9, 2005, 11:38:30 ; Search time 42 Seconds  
(without alignments)  
956.219 Million cell updates/sec

Title: US-10-620-169-4  
Perfect score: 2958  
Sequence: 1 MPRGWAAPLLLLLQGGWCC.....YLRQWVPPPLSSFPQAS 538

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: /cgn2\_6/prodata/1/iaa/5B COMB.pep:\*\*
- 3: /cgn2\_6/prodata/1/iaa/6A COMB.pep:\*\*
- 4: /cgn2\_6/prodata/1/iaa/6B COMB.pep:\*\*
- 5: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep:\*\*
- 6: /cgn2\_6/prodata/1/iaa/backfiles1.pcp:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	2958	100.0	538	3 US-09-040-005-2	Sequence 2, Appli
2	2958	100.0	538	3 US-09-522-217-115	Sequence 115, App
3	2958	100.0	538	4 US-09-404-641-2	Sequence 2, Appli
4	2958	100.0	538	4 US-09-923-246-115	Sequence 115, App
5	2958	100.0	538	4 US-10-295-723-115	Sequence 115, App
6	2958	100.0	538	4 US-10-414-186-2	Sequence 2, Appli
7	2958	100.0	538	4 US-09-825-561A-2	Sequence 2, Appli
8	2958	100.0	538	4 US-10-243-072-2	Sequence 2, Appli
9	2958	100.0	547	4 US-09-949-016-11544	Sequence 11544, A
10	2817	95.2	568	4 US-09-825-561A-65	Sequence 65, Appl
11	1735.5	58.7	529	4 US-09-404-641-85	Sequence 85, Appl
12	1735.5	58.7	529	4 US-10-414-186-85	Sequence 85, Appl
13	1735.5	58.7	529	4 US-09-825-561A-12	Sequence 12, Appl
14	1735.5	58.7	529	4 US-10-243-072-85	Sequence 85, Appl
15	1729.5	58.5	529	4 US-09-732-234-6	Sequence 6, Appli
16	1729.5	58.5	529	4 US-09-784-859-6	Sequence 16, Appl
17	1302	44.0	567	4 US-09-825-561A-16	Sequence 81, Appl
18	1221.5	41.3	397	4 US-09-404-641-81	Sequence 81, Appl
19	1221.5	41.3	397	4 US-10-243-072-81	Sequence 81, Appl
20	1221.5	41.3	397	4 US-10-243-072-81	Sequence 81, Appl
21	1197	40.5	606	3 US-09-522-217-97	Sequence 97, Appl
22	1197	40.5	606	4 US-09-404-641-51	Sequence 51, Appl
23	1197	40.5	606	4 US-09-923-246-97	Sequence 97, Appl
24	1197	40.5	606	4 US-10-295-723-97	Sequence 97, Appl
25	1197	40.5	606	4 US-10-414-186-51	Sequence 51, Appl
26	1197	40.5	606	4 US-09-825-561A-30	Sequence 30, Appl
27	1197	40.5	606	4 US-10-243-072-51	Sequence 51, Appl

28 1195 40.4 218 4 US-09-825-561A-6 Sequence 6, Appli

29 1135 38.4 261 4 US-09-825-561A-71 Sequence 71, Appl

30 1100 37.2 247 4 US-09-825-561A-69 Sequence 69, Appl

31 844 28.5 486 4 US-09-825-561A-73 Sequence 73, Appl

32 677.5 22.9 240 4 US-09-404-641-70 Sequence 70, Appl

33 677.5 22.9 240 4 US-10-414-186-70 Sequence 70, Appl

34 677.5 22.9 240 4 US-10-243-072-70 Sequence 70, Appl

35 278 9.4 551 3 US-09-194-145-2 Sequence 2, Appli

36 278 9.4 551 6 5198359-2 Patent No. 5198359

37 278 9.4 551 6 549756-2 Patent No. 549756

38 278 9.4 551 6 5198359-2 Patent No. 5198359

39 278 9.4 551 6 549756-2 Patent No. 549756

40 248.5 8.4 539 6 549756-4 Patent No. 549756

41 248.5 8.4 539 6 549756-4 Patent No. 549756

42 247.5 8.4 539 6 5198359-4 Patent No. 5198359

43 247.5 8.4 539 6 5198359-4 Patent No. 5198359

44 231 7.8 536 4 US-09-949-016-8560 Sequence 8560, Ap

45 220.5 7.5 468 1 US-08-164-614A-7 Sequence 7, Appli

## ALIGNMENTS

RESULT 1  
US-09-040-005-2  
; Sequence 2, Application US/09040005  
; Patent No. 6057128  
; GENERAL INFORMATION:  
; APPLICANT: Donaldson, Debra  
; APPLICANT: Unger, Michelle  
; TITLE OF INVENTION: MU-1 RECEPTOR  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 Cambridgepark Drive  
; CITY: Cambridge  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/040,005  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A  
; REGISTRATION NUMBER: 32,724  
; REFERENCE/DOCKET NUMBER: G15320  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-498-8224  
; TELEFAX: 617-876-5851  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 538 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-040-005-2

Query Match 100.0%; Score 2958; DB 3; Length 538;  
Best Local Similarity 100.0%; Pred. No. 3e-266;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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## RESULT 2

US-09-522-217-115  
; Sequence 115, Application US/09522217  
; Patent No. 6307024  
; GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Foster, Donald D.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Gross, Jane A.  
; APPLICANT: Johnston, Janet V.  
; APPLICANT: Nelson, Andrew J.  
; APPLICANT: Dillon, Stacey R.  
; APPLICANT: Hammond, Angela K.  
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND  
; FILE REFERENCE: 99-16  
; CURRENT APPLICATION NUMBER: US/09/522,217  
; PRIOR FILING DATE: 2000-03-09  
; EARLIER APPLICATION NUMBER: US 60/123,547  
; EARLIER FILING DATE: 1999-03-09  
; EARLIER APPLICATION NUMBER: US 60/123,904  
; EARLIER FILING DATE: 1999-03-11  
; EARLIER APPLICATION NUMBER: US 60/142,013  
; EARLIER FILING DATE: 1999-07-01  
; NUMBER OF SEQ ID NOS: 115  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 115  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens

## US-09-522-217-115

Query Match 100.0%; Score 2958; DB 3; Length 538;  
Best Local Similarity 100.0%; Pred. No. 3e-266;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 EATSCSLHRSAHNATHATYTCMDVFFHFMADDIFSVNITDQSGNYSQECGFLLAESIKP 120  
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## RESULT 3

US-09-404-641-2  
; Sequence 2, Application US/09404641  
; Patent No. 6576744  
; GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.  
; APPLICANT: Conklin, Darrell C.  
; APPLICANT: No. 6576744ak, Julia E.  
; APPLICANT: Hammond, Angela K.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLH11  
; FILE REFERENCE: 98-55  
; CURRENT APPLICATION NUMBER: US/09/404,641  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: US 60/100,896  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: US 60/123,546  
; PRIOR FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: US 60/142,574  
; PRIOR FILING DATE: 1999-07-06  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens

## US-09-404-641-2

Query Match 100.0%; Score 2958; DB 4; Length 538;  
Best Local Similarity 100.0%; Pred. No. 3e-266;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGWAAPLLLLLLQGGGCPDLVCYTDYLOTVICILEMNLHPSTLTLTWQDQYEELKD 60  
Db 1 MPRGWAAPLLLLLLQGGGCPDLVCYTDYLOTVICILEMNLHPSTLTLTWQDQYEELKD 60

QY 61 EATSCSLHRSAHNATHATYTCMDVFFHFMADDIFSVNITDQSGNYSQECGFLLAESIKP 120  
Db 61 EATSCSLHRSAHNATHATYTCMDVFFHFMADDIFSVNITDQSGNYSQECGFLLAESIKP 120  
QY 121 APPFNVTTFSGQYNIWSRSDYEDPAFYMLKGKLOLQYELQYRNRGDPWAVSPRRKLIISVDS 180

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Db 121 APPFNVTTFSGQYNIWSRSDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRRKLISVDS 180
Qy 181 RVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIFQTSBELKEGWNPHLL 240
Db 181 RVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIFQTSBELKEGWNPHLL 240
Qy 241 LLLLVIVIPAFWSLTKTHPLWRLWKKIWAVSPERFPMPLYKGCSDGPKKWWGAPFTGSS 300
Db 241 LLLLVIVIPAFWSLTKTHPLWRLWKKIWAVSPERFPMPLYKGCSDGPKKWWGAPFTGSS 300
Qy 301 LELGWSPEVSTLEVISCHPPRSPAKRLQLTELQEPALVESDGVKPSFWMPTAQNCG 360
Db 301 LELGWSPEVSTLEVISCHPPRSPAKRLQLTELQEPALVESDGVKPSFWMPTAQNCG 360
Qy 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLADGLESPGLDPLLD 420
Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLADGLESPGLDPLLD 420
Qy 421 AGTTVLSCGVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSSEAGS 480
Db 421 AGTTVLSCGVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSSEAGS 480
Qy 481 FLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538
Db 481 FLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538
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## RESULT 4

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US-09-923-246-115
; Sequence 115, Application US/09923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E.
; APPLICANT: Preenell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-246-115
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Query Match 100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 3e-266;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MPRGWAAPLLLLLQGGWCPDLVCYTDYLTQVICILEMNLHPSLTTLTWQDQYEELKD 60
Db 1 MPRGWAAPLLLLLQGGWCPDLVCYTDYLTQVICILEMNLHPSLTTLTWQDQYEELKD 60
Qy 61 EATCSLHRSAHNATHATYTCMDVHFPMADDIFSVNITDQSGNYSQEGSFLAESIKP 120
Db 61 EATCSLHRSAHNATHATYTCMDVHFPMADDIFSVNITDQSGNYSQEGSFLAESIKP 120
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Qy 121 APPFNVTTFSGQYNIWSRSDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRRKLISVDS 180
Db 121 APPFNVTTFSGQYNIWSRSDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRRKLISVDS 180
Qy 181 RVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIFQTSBELKEGWNPHLL 240
Db 181 RVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIFQTSBELKEGWNPHLL 240
Qy 241 LLLLVIVIPAFWSLTKTHPLWRLWKKIWAVSPERFPMPLYKGCSDGPKKWWGAPFTGSS 300
Db 241 LLLLVIVIPAFWSLTKTHPLWRLWKKIWAVSPERFPMPLYKGCSDGPKKWWGAPFTGSS 300
Qy 301 LELGWSPEVSTLEVISCHPPRSPAKRLQLTELQEPALVESDGVKPSFWMPTAQNCG 360
Db 301 LELGWSPEVSTLEVISCHPPRSPAKRLQLTELQEPALVESDGVKPSFWMPTAQNCG 360
Qy 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLADGLESPGLDPLLD 420
Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLADGLESPGLDPLLD 420
Qy 421 AGTTVLSCGVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSSEAGS 480
Db 421 AGTTVLSCGVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSSEAGS 480
Qy 481 FLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538
Db 481 FLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538
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## RESULT 5

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US-10-295-723-115
; Sequence 115, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: No. 6686178ak, Julia E.
; APPLICANT: Preenell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-723-115
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Query Match 100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 3e-266;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MPRGWAAPLLLLLQGGWCPDLVCYTDYLTQVICILEMNLHPSLTTLTWQDQYEELKD 60
Db 1 MPRGWAAPLLLLLQGGWCPDLVCYTDYLTQVICILEMNLHPSLTTLTWQDQYEELKD 60
Qy 61 EATCSLHRSAHNATHATYTCMDVHFPMADDIFSVNITDQSGNYSQEGSFLAESIKP 120
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Db 61 EATCSLHRSAHNATHATYTCMDVFHFMADDIFSVNITDQSGNYSQCGSFLAESIKP 120  
Qy 121 APPENVTVTFSGQYNI SWRSYEDPAFYMLKGKLOQYELQYRNRGDPWAVSPRRKLISVDS 180  
Db 121 APPENVTVTFSGQYNI SWRSYEDPAFYMLKGKLOQYELQYRNRGDPWAVSPRRKLISVDS 180  
Qy 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVI FOTQSEELKEGWNPHLLL 240  
Db 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVI FOTQSEELKEGWNPHLLL 240  
Qy 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVI FOTQSEELKEGWNPHLLL 240  
Db 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVI FOTQSEELKEGWNPHLLL 240  
Qy 241 LLLLVIVIFAFWLSKTHPLRLWKKI WAVSPERFFMPLYKGCSDGPKKVVGAFFTGSS 300  
Db 241 LLLLVIVIFAFWLSKTHPLRLWKKI WAVSPERFFMPLYKGCSDGPKKVVGAFFTGSS 300  
Qy 301 LELGWSPEVSTLEVYCHPPSPAKRLQLTQLQEPALVESDGVKPKSFWPTAQNSSG 360  
Db 301 LELGWSPEVSTLEVYCHPPSPAKRLQLTQLQEPALVESDGVKPKSFWPTAQNSSG 360  
Qy 361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDLDAGLEPSGLEDPLLD 420  
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDLDAGLEPSGLEDPLLD 420  
Qy 421 AGTTVLSGCVSAGSGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480  
Db 421 AGTTVLSGCVSAGSGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480  
Qy 481 PLAGLDMDTFDSGFVSGDCSPVECDFTSPGDEGPPRSYLQWVVI PPPLSSPGQAS 538  
Db 481 PLAGLDMDTFDSGFVSGDCSPVECDFTSPGDEGPPRSYLQWVVI PPPLSSPGQAS 538

RESULT 7  
US-09-825-561A-2  
; Sequence 2, Application US/09825561A  
; Patent No. 6777539  
; GENERAL INFORMATION:  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: No. 6777539ak, Julia E.  
; APPLICANT: West, James W.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Nelson, Andrew J.  
; TITLE OF INVENTION: SOLUBLE ZALPHAIL CYTOKINE RECEPTORS  
; FILE REFERENCE: 00-22  
; CURRENT APPLICATION NUMBER: US/09/825,561A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/194,731  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/222,121  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 86  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-825-561A-2

Query Match 100.0%; Score 2958; DB 4; Length 538;  
Best Local Similarity 100.0%; Pred. No. 3e-266;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MPRGWAAPLLLLLQGGWCPDLVCYTDYLTQTVICILEMNLHPSTLTLTWQDQYEELKD 60  
Db 1 MPRGWAAPLLLLLQGGWCPDLVCYTDYLTQTVICILEMNLHPSTLTLTWQDQYEELKD 60  
Qy 61 EATCSLHRSAHNATHATYTCMDVFHFMADDIFSVNITDQSGNYSQCGSFLAESIKP 120  
Db 61 EATCSLHRSAHNATHATYTCMDVFHFMADDIFSVNITDQSGNYSQCGSFLAESIKP 120  
Qy 121 APPENVTVTFSGQYNI SWRSYEDPAFYMLKGKLOQYELQYRNRGDPWAVSPRRKLISVDS 180  
Db 121 APPENVTVTFSGQYNI SWRSYEDPAFYMLKGKLOQYELQYRNRGDPWAVSPRRKLISVDS 180  
Qy 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVI FOTQSEELKEGWNPHLLL 240

Db 61 EATCSLHRSAHNATHATYTCMDVFHFMADDIFSVNITDQSGNYSQCGSFLAESIKP 120  
Qy 121 APPENVTVTFSGQYNI SWRSYEDPAFYMLKGKLOQYELQYRNRGDPWAVSPRRKLISVDS 180  
Db 121 APPENVTVTFSGQYNI SWRSYEDPAFYMLKGKLOQYELQYRNRGDPWAVSPRRKLISVDS 180  
Qy 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVI FOTQSEELKEGWNPHLLL 240  
Db 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVI FOTQSEELKEGWNPHLLL 240  
Qy 241 LLLLVIVIFAFWLSKTHPLRLWKKI WAVSPERFFMPLYKGCSDGPKKVVGAFFTGSS 300  
Db 241 LLLLVIVIFAFWLSKTHPLRLWKKI WAVSPERFFMPLYKGCSDGPKKVVGAFFTGSS 300  
Qy 301 LELGWSPEVSTLEVYCHPPSPAKRLQLTQLQEPALVESDGVKPKSFWPTAQNSSG 360  
Db 301 LELGWSPEVSTLEVYCHPPSPAKRLQLTQLQEPALVESDGVKPKSFWPTAQNSSG 360  
Qy 361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDLDAGLEPSGLEDPLLD 420  
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDLDAGLEPSGLEDPLLD 420  
Qy 421 AGTTVLSGCVSAGSGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480  
Db 421 AGTTVLSGCVSAGSGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480  
Qy 481 PLAGLDMDTFDSGFVSGDCSPVECDFTSPGDEGPPRSYLQWVVI PPPLSSPGQAS 538  
Db 481 PLAGLDMDTFDSGFVSGDCSPVECDFTSPGDEGPPRSYLQWVVI PPPLSSPGQAS 538

RESULT 6  
US-10-414-186-2  
; Sequence 2, Application US/10414186  
; Patent No. 6692924  
; GENERAL INFORMATION:  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Conklin, Darrell C.  
; APPLICANT: No. 6692924ak, Julia E.  
; APPLICANT: Hammond, Angela K.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZALPHAIL  
; FILE REFERENCE: 98-55  
; CURRENT APPLICATION NUMBER: US/10/414,186  
; CURRENT FILING DATE: 2003-04-14  
; PRIOR APPLICATION NUMBER: US/09/404,641  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-414-186-2

Query Match 100.0%; Score 2958; DB 4; Length 538;  
Best Local Similarity 100.0%; Pred. No. 3e-266;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MPRGWAAPLLLLLQGGWCPDLVCYTDYLTQTVICILEMNLHPSTLTLTWQDQYEELKD 60  
Db 1 MPRGWAAPLLLLLQGGWCPDLVCYTDYLTQTVICILEMNLHPSTLTLTWQDQYEELKD 60  
Qy 61 EATCSLHRSAHNATHATYTCMDVFHFMADDIFSVNITDQSGNYSQCGSFLAESIKP 120  
Db 61 EATCSLHRSAHNATHATYTCMDVFHFMADDIFSVNITDQSGNYSQCGSFLAESIKP 120

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Db 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVI FQTQSEBELKEGWNPHLLL 240
Qy 241 LLLLVIVIFAPFWSLTKTHPLRLWKIWA VSPERFFMPLYKGCSDGDFKWKVGAFTGSS 300
Db 241 LLLLVIVIFAPFWSLTKTHPLRLWKIWA VSPERFFMPLYKGCSDGDFKWKVGAFTGSS 300
Qy 301 LELGWSPEVSTLEVISCHPSPRPAKRLQ LTELQEPALVESDGVKPSFWPTAQN SGG 360
Db 301 LELGWSPEVSTLEVISCHPSPRPAKRLQ LTELQEPALVESDGVKPSFWPTAQN SGG 360
Qy 361 SAYSEERDRPYGLVSDITVTVLDAEGPCT WPCSCDDGYPALDL DLAGLEPSGLDPLLD 420
Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCT WPCSCDDGYPALDL DLAGLEPSGLDPLLD 420
Qy 421 AGTTLVSCGCVSAGSPGLGGLSLDLRLK PPLADGEDWAGGLPWGGRSPGVSSEAGS 480
Db 421 AGTTLVSCGCVSAGSPGLGGLSLDLRLK PPLADGEDWAGGLPWGGRSPGVSSEAGS 480
Qy 481 PLAGLDMDTDFSGFVSGDCSSPVECDFTS PGDEGPPRSYLRQWVVI PPLSPGPQAS 538
Db 481 PLAGLDMDTDFSGFVSGDCSSPVECDFTS PGDEGPPRSYLRQWVVI PPLSPGPQAS 538
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## RESULT 8

US-10-243-072-2

; Sequence 2, Application US/10243072

; Patent No. 6803451

; GENERAL INFORMATION:

; APPLICANT: Prenelli, Scott R.

; APPLICANT: Conklin, Barrrell C.

; APPLICANT: No. 6803451ak, Julia E.

; APPLICANT: Hammond, Angela K.

; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL

; FILE REFERENCE: 98-55C1

; CURRENT APPLICATION NUMBER: US/10/243,072

; CURRENT FILING DATE: 2002-09-13

; PRIOR APPLICATION NUMBER: 09/628,127

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: US 60/100,896

; PRIOR FILING DATE: 1998-09-23

; PRIOR APPLICATION NUMBER: US 60/123,546

; PRIOR FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: US 60/142,574

; PRIOR FILING DATE: 1999-07-06

; PRIOR APPLICATION NUMBER: US 09/404,641

; PRIOR FILING DATE: 1999-09-23

; NUMBER OF SEQ ID NOS: 92

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 538

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-243-072-2

Query Match 100.0%; Score 2958; DB 4; Length 538;

Best Local Similarity 100.0%; Pred. No. 3e-266;

Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MPRGWAAPLLLLLLQGGWGCPLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60
Db 1 MPRGWAAPLLLLLLQGGWGCPLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60
Qy 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSCQGSFLLAESIKP 120
Db 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSCQGSFLLAESIKP 120
Qy 121 APPNVNVTTFSGQYNISWRSDYEDPAFYMLKGKQLQYELQYNRGDPWAVSPRRKLISVDS 180
Db 121 APPNVNVTTFSGQYNISWRSDYEDPAFYMLKGKQLQYELQYNRGDPWAVSPRRKLISVDS 180
Qy 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVI FQTQSEBELKEGWNPHLLL 240
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Db 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVI FQTQSEBELKEGWNPHLLL 240
Qy 241 LLLLVIVIFAPFWSLTKTHPLRLWKIWA VSPERFFMPLYKGCSDGDFKWKVGAFTGSS 300
Db 241 LLLLVIVIFAPFWSLTKTHPLRLWKIWA VSPERFFMPLYKGCSDGDFKWKVGAFTGSS 300
Qy 301 LELGWSPEVSTLEVISCHPSPRPAKRLQ LTELQEPALVESDGVKPSFWPTAQN SGG 360
Db 301 LELGWSPEVSTLEVISCHPSPRPAKRLQ LTELQEPALVESDGVKPSFWPTAQN SGG 360
Qy 361 SAYSEERDRPYGLVSDITVTVLDAEGPCT WPCSCDDGYPALDL DLAGLEPSGLDPLLD 420
Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCT WPCSCDDGYPALDL DLAGLEPSGLDPLLD 420
Qy 421 AGTTLVSCGCVSAGSPGLGGLSLDLRLK PPLADGEDWAGGLPWGGRSPGVSSEAGS 480
Db 421 AGTTLVSCGCVSAGSPGLGGLSLDLRLK PPLADGEDWAGGLPWGGRSPGVSSEAGS 480
Qy 481 PLAGLDMDTDFSGFVSGDCSSPVECDFTS PGDEGPPRSYLRQWVVI PPLSPGPQAS 538
Db 481 PLAGLDMDTDFSGFVSGDCSSPVECDFTS PGDEGPPRSYLRQWVVI PPLSPGPQAS 538
```

## RESULT 9

US-09-949-016-11544

; Sequence 11544, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 11544

; LENGTH: 547

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-11544

Query Match 100.0%; Score 2958; DB 4; Length 547;

Best Local Similarity 100.0%; Pred. No. 3.1e-266;

Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MPRGWAAPLLLLLLQGGWGCPLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60
Db 10 MPRGWAAPLLLLLLQGGWGCPLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 69
Qy 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSCQGSFLLAESIKP 120
Db 70 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSCQGSFLLAESIKP 129
Qy 121 APPNVNVTTFSGQYNISWRSDYEDPAFYMLKGKQLQYELQYNRGDPWAVSPRRKLISVDS 180
Db 130 APPNVNVTTFSGQYNISWRSDYEDPAFYMLKGKQLQYELQYNRGDPWAVSPRRKLISVDS 189
Qy 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVI FQTQSEBELKEGWNPHLLL 240
Db 190 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVI FQTQSEBELKEGWNPHLLL 249
Qy 241 LLLLVIVIFAPFWSLTKTHPLRLWKIWA VSPERFFMPLYKGCSDGDFKWKVGAFTGSS 300
Db 250 LLLLVIVIFAPFWSLTKTHPLRLWKIWA VSPERFFMPLYKGCSDGDFKWKVGAFTGSS 309
Qy 301 LELGWSPEVSTLEVISCHPSPRPAKRLQ LTELQEPALVESDGVKPSFWPTAQN SGG 360
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Db 310 LELGPMSEVSTLEVSCHPPSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSGG 369  
Qy 361 SAYSEERDRPYGLVSIIDVTVLDAEGPCTWPCSCEDDGYPALDLDAGLEPSPGLEPDL 420  
Db 370 SAYSEERDRPYGLVSIIDVTVLDAEGPCTWPCSCEDDGYPALDLDAGLEPSPGLEPDL 429  
Qy 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
Db 430 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 489  
Qy 481 PLAGLDMDTFDSGFGVSCSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 538  
Db 490 PLAGLDMDTFDSGFGVSCSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 547

## RESULT 10

US-09-825-561A-65

; Sequence 65, Application US/09825561A

; Patent No. 6777539

; GENERAL INFORMATION:

; APPLICANT: Sprecher, Cindy A.

; APPLICANT: No. 6777539ak, Julia E.

; APPLICANT: West, James W.

; APPLICANT: Presnell, Scott R.

; APPLICANT: Holly, Richard D.

; APPLICANT: Nelson, Andrew J.

; TITLE OF INVENTION: SOLUBLE ZAPLHALL CYTOKINE RECEPTORS

; FILE REFERENCE: 00-22

; CURRENT APPLICATION NUMBER: US/09/825,561A

; CURRENT FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 60/194,731

; PRIOR FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 60/222,121

; PRIOR FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 86

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 65

; LENGTH: 568

; TYPE: PRT

; ORGANISM: homo sapiens

; US-09-825-561A-65

Query Match 95.2%; Score 2817; DB 4; Length 568;  
Best Local Similarity 89.9%; Pred. No. 4.3e-253;  
Matches 523; Conservative 0; Mismatches 1; Indels 58; Gaps 3;

Qy 1 MPRGWAAPLLLLLQGG-----GMGCPDLVCYTDYLTQVI 34  
Db 1 MPRGWAAPLLLLLQGGALGEMERKLCSPKPPPTKASLPDTPPGMGCPDLVCYTDYLTQVI 60  
Qy 35 CILEMNNLHPSTLTITW-----QOYEELKDBATSCSLHRSNAATH 76  
Db 61 CILEMNNLHPSTLTITWLSNNTGCIKDRTLDLRQOYEELKDBATSCSLHRSNAATH 120  
Qy 77 ATYTCHMDVHFHMADDFSVNITDQSGNYSCGSEFLAESIKPAPPENVTTFSGQNI 136  
Db 121 ATYTCHMDVHFHMADDFSVNITDQSGNYSCGSEFLAE-----SRQNI 166  
Qy 137 SWRSYEDPAFYMLKGKLOYLQYLRNRGDPWAVSPRRKLI1SVDSRSVLLPLEFRKSSY 196  
Db 167 SWRSYEDPAFYMLKGKLOYLQYLRNRGDPWAVSPRRKLI1SVDSRSVLLPLEFRKSSY 226  
Qy 197 ELQVRAGMPGSSYOGTWSWSDPVI FQTSBELKEGNPHLLLLLLLVIFIPAFWSLK 256  
Db 227 ELQVRAGMPGSSYOGTWSWSDPVI FQTSBELKEGNPHLLLLLLLVIFIPAFWSLK 286  
Qy 257 THPLWRLWKKIWA VPSPERFPMPLYKCGDGFKKWVGAPFTGSSLELGPWSEVPSTLEV 316  
Db 287 THPLWRLWKKIWA VPSPERFPMPLYKCGDGFKKWVGAPFTGSSLELGPWSEVPSTLEV 346  
Qy 317 YSCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSGG SAYSEERDRPYGLVSI 376

Db 347 YSCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSGG SAYSEERDRPYGLVSI 406  
Qy 377 DTVTVLDAEGPCTWPCSCEDDGYPALDLDAGLEPSPGLEPDLDAAGTTVLSCGCVSAGSP 436  
Db 407 DTVTVLDAEGPCTWPCSCEDDGYPALDLDAGLEPSPGLEPDLDAAGTTVLSCGCVSAGSP 466  
Qy 437 GLGGPLASLLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGSPLAGLDMDTFDSGFVG 496  
Db 467 GLGGPLASLLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGSPLAGLDMDTFDSGFVG 526  
Qy 497 SDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 538  
Db 527 SDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 568

## RESULT 11

US-09-404-641-85

; Sequence 85, Application US/09404641

; Patent No. 6576744

; GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.

; APPLICANT: Conklin, Darrell C.

; APPLICANT: No. 6576744ak, Julia E.

; APPLICANT: Hammond, Angela K.

; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL

; FILE REFERENCE: 98-55

; CURRENT APPLICATION NUMBER: US/09/404,641

; CURRENT FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/100,896

; PRIOR FILING DATE: 1998-09-23

; PRIOR APPLICATION NUMBER: US 60/123,546

; PRIOR FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: US 60/142,574

; PRIOR FILING DATE: 1999-07-06

; NUMBER OF SEQ ID NOS: 91

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 85

; LENGTH: 529

; TYPE: PRT

; ORGANISM: Mus musculus

; US-09-404-641-85

Query Match 58.7%; Score 1735.5; DB 4; Length 529;  
Best Local Similarity 62.7%; Pred. No. 1.5e-152;  
Matches 340; Conservative 49; Mismatches 136; Indels 17; Gaps 6;

Qy 1 MPRGWAAPLLLLLQGGCPDLVCYTDYLTQVI CILEMNNLHPSTLTITWQOYEELKD 60  
Db 1 MPRGFWAALLLLHGAWSCLDLTCYTDYLTWITTCVLETRSPNPSILSLTWQOYEELQD 60  
Qy 61 EATSCSLHRSNAATHATYTCHMDVHFHMADDFSVNITDQSGNYSCGSEFLAESIKP 120  
Db 61 QETCSLHRSNGHTHTIWTCHMRLSQPLSDEVIVNVTQSGNNSQCGSFVLAESIKP 120  
Qy 121 APPENVTTFSGQNI1SWRSYEDPAFYMLKGKLOYLQYLRNRGDPWAVSPRRKLI1SVDS 180  
Db 121 APPLNVTVAFSGRYD1SWDSAYDEPSNYLRGLQYELQYLRNLRDPYAVRPVTKLI1SVDS 180  
Qy 181 RSVSLLPLEFRKSSYELQVRAGMPGSSYOGTWSWSDPVI FQTSBELKEGNPHLL 240  
Db 181 RNVSLLPEEFKDSY1QLQVRAAPQPGTSPFGTWSWSDPVI FQTSBELKEGNPHLL 240  
Qy 241 LLLLVIVIFIPAFWSLKTHPLWRLWKKIWA-VPSPERFPMPLYKCGDGFKKWVGAPFTGS 299  
Db 241 LLAVLIIVL-VFMGLKTHPLWRLWKKIWA VPTPESFQPLYREHSGNFKKWVTPFTAS 299  
Qy 300 SLELGPWSEVPSTLEVYVYCHPPRSPAKRLQLTELQEPALVESDGVKPSFW---PTAQ 356  
Db 300 SIELVQSSSTTSAL-----HLSLYPAKEKFPGLGLEQLECDGMSEPGHWCIIPLAA 354  
Qy 357 NSGGSAYSEERDRPYGLVSIIDVTVLDAEGPCTWPCSCEDDGYPALDLDAGLEPSPGLE 416  
Db 355 QGAVSAYSEERDRPYGLVSIIDVTVGDAEGLCVWPCSCEDDGYFAMNLDAGRESGPNSED 414

QY 417 PLLDAGTTVLSCGCVSAGSPGLGGLGSLDLRLKPLADGEDWAGGLPMGGRSPGVSSES 476  
DB 415 LLLVTDPAFLSCGCVSAGSPGLGGLGSLDLRLKPLADGEDWAGGLPMGGRSPGVSSES 474  
QY 477 EAGSPLAGLMDTDFDSGFGVSGDCSSPVECDFTSPGDBGPPRSYLROWVVIIPPLSSPGPO 536  
DB 475 EAGSP-PGLMDTDFDSGFGVSGDCSSPVECDFTSPGDBGPPRSYLROWVVIIPPLSSPGPO 527  
QY 537 AS 538  
DB 528 SS 529

## RESULT 12

US-10-414-186-85  
; Sequence 85, Application US/10414186  
; Patent No. 6692924  
; GENERAL INFORMATION:  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Conklin, Darrell C.  
; APPLICANT: No. 6692924ak, Julia E.  
; APPLICANT: Hammond, Angela K.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL  
; FILE REFERENCE: 98-55  
; CURRENT APPLICATION NUMBER: US/10/414,186  
; PRIOR FILING DATE: 2003-04-14  
; PRIOR APPLICATION NUMBER: US/09/404,641  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 85  
; LENGTH: 529  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-414-186-85

Query Match 58.7%; Score 1735.5; DB 4; Length 529;  
Best Local Similarity 62.7%; Pred. No. 1.5e-152;  
Matches 340; Conservative 49; Mismatches 136; Indels 17; Gaps 6;

QY 1 MPRGWAAPLLLLLOGGCGCPDLVCYTDYLOTVICILEMNLHPSTLTLTWQDOYEELKD 60  
DB 1 MPRGVAALLLLILHGAWSCDLTCTYDYLTTTCLVLETRSPNPSILSLTWODEYEELQD 60  
QY 61 EATCSLHRSAHNATHATYTCMDVFFHFMADDIFSVNITDQSGNYSQCGSPFLAESIKP 120  
DB 61 QETFCSLHRSAGHNTTHIWTCHMLRSQFLSDEVFVNVTDQSGNYSQCGSPFLAESIKP 120  
QY 121 APPFNVTTFSGQWNISWRSDYEDPAFMYLKGKQLQYELQYLRNRGDPWAPRKLISVDS 180  
DB 121 APPLNVTVAFSGRYDISWDSAYDEPSNYVLRGKQLQYELQYLRNLRDPYAVRPVTKLISVDS 180  
QY 181 RSVSLPLLEFRKDSYELQVRAGPMGSSYQGTWSESDPVTFOQSEELKEGNPHLL 240  
DB 181 RNVSLLPEEFKDKSSYQLQVRAAPQGTSGFRGTWSESDPVTFOQAGEPEAGNDPHMLL 240  
QY 241 LLLLVITFPAFWSLTKTHPLRLWKIWA-VPSPERFFMPLYKGCSDGPKKVVGAPFTGS 299  
DB 241 LLAVLIIVL-VFMGLKIHLPRLWKIWA-PVTPESFPQPLYREHSGNFKKWNTPFTAS 299  
QY 300 SLELGPWSPVSTLEVSCHPPRPAKRLQLTQELQEPALVESDGVKPKPSFW---PTAQ 356  
DB 300 SIELVQSSSTTTTSALE----HLSLYPAKEKPPGLGLEEQLECDGMESEPGHWCIIPLAA 354  
QY 357 NSGGSAYSEERDRPYGLVSIIDTVTDAGPCTWPCSCDDGYPALDLDAGLEPSPGLE 416

DB 355 GOAVSAYSEERDRPYGLVSIIDTVTDAGLEGLCWPCSCDDGYPAMNLDAGRESGPNSED 414  
QY 417 PLLDAGTTVLSCGCVSAGSPGLGGLGSLDLRLKPLADGEDWAGGLPMGGRSPGVSSES 476  
DB 415 LLLVTDPAFLSCGCVSAGSPGLGGLGSLDLRLKPLADGEDWAGGLPMGGRSPGVSSES 474  
QY 477 EAGSPLAGLMDTDFDSGFGVSGDCSSPVECDFTSPGDBGPPRSYLROWVVIIPPLSSPGPO 536  
DB 475 EAGSP-PGLMDTDFDSGFGVSGDCSSPVECDFTSPGDBGPPRSYLROWVVIIPPLSSPGPO 527  
QY 537 AS 538  
DB 528 SS 529

## RESULT 13

US-09-825-561A-12  
; Sequence 12, Application US/09825561A  
; Patent No. 677539  
; GENERAL INFORMATION:  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: No. 677539ak, Julia E.  
; APPLICANT: West, James W.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Nelson, Andrew J.  
; TITLE OF INVENTION: SOLUBLE ZAPLHALL CYTOKINE RECEPTORS  
; FILE REFERENCE: 00-22  
; CURRENT APPLICATION NUMBER: US/09/825,561A  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/194,731  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/222,121  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 86  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 529  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-825-561A-12

Query Match 58.7%; Score 1735.5; DB 4; Length 529;  
Best Local Similarity 62.7%; Pred. No. 1.5e-152;  
Matches 340; Conservative 49; Mismatches 136; Indels 17; Gaps 6;

QY 1 MPRGWAAPLLLLLOGGCGCPDLVCYTDYLOTVICILEMNLHPSTLTLTWQDOYEELKD 60  
DB 1 MPRGVAALLLLILHGAWSCDLTCTYDYLTTTCLVLETRSPNPSILSLTWODEYEELQD 60  
QY 61 EATCSLHRSAHNATHATYTCMDVFFHFMADDIFSVNITDQSGNYSQCGSPFLAESIKP 120  
DB 61 QETFCSLHRSAGHNTTHIWTCHMLRSQFLSDEVFVNVTDQSGNYSQCGSPFLAESIKP 120  
QY 121 APPFNVTTFSGQWNISWRSDYEDPAFMYLKGKQLQYELQYLRNRGDPWAPRKLISVDS 180  
DB 121 APPLNVTVAFSGRYDISWDSAYDEPSNYVLRGKQLQYELQYLRNLRDPYAVRPVTKLISVDS 180  
QY 181 RSVSLPLLEFRKDSYELQVRAGPMGSSYQGTWSESDPVTFOQSEELKEGNPHLL 240  
DB 181 RNVSLLPEEFKDKSSYQLQVRAAPQGTSGFRGTWSESDPVTFOQAGEPEAGNDPHMLL 240  
QY 241 LLLLVITFPAFWSLTKTHPLRLWKIWA-VPSPERFFMPLYKGCSDGPKKVVGAPFTGS 299  
DB 241 LLAVLIIVL-VFMGLKIHLPRLWKIWA-PVTPESFPQPLYREHSGNFKKWNTPFTAS 299  
QY 300 SLELGPWSPVSTLEVSCHPPRPAKRLQLTQELQEPALVESDGVKPKPSFW---PTAQ 356  
DB 300 SIELVQSSSTTTTSALE----HLSLYPAKEKPPGLGLEEQLECDGMESEPGHWCIIPLAA 354  
QY 357 NSGGSAYSEERDRPYGLVSIIDTVTDAGPCTWPCSCDDGYPALDLDAGLEPSPGLE 416  
DB 355 GOAVSAYSEERDRPYGLVSIIDTVTDAGLEGLCWPCSCDDGYPAMNLDAGRESGPNSED 414



Qy	477	EAGSLAGLDMDTFDSGFVSGDCSPVRCDFTSPCDEGPPRSYLRQWVVI	PPPLSSPCPQ	536
Db	475	EAGSP-PGLDMDTFDSGFAGSDCGSPVET-----DEGPPRSYLRQWVVRT	PPVDSGAQ	527
Qy	537	AS	538	
Db	528	SS	529	

Search completed: July 9, 2005, 11:48:39  
Job time : 44 secs

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OM protein - protein search, using sw model

Run on: July 9, 2005, 11:44:05 ; Search time 65 Seconds  
(without alignments)  
1080.022 Million cell updates/sec

Title: US-10-620-169-4  
Perfect score: 2958  
Sequence: 1 MPRGWAAPLLILLQGWGC.....YLRQWVTPPLSSFPQAS 538

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 614041 seqs, 130485892 residues

Total number of hits satisfying chosen parameters: 614041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents AA New.\*  
1: /cgn2\_6/prodata/2/paa/PCT\_NEW\_COMB.pep.\*  
2: /cgn2\_6/prodata/2/paa/US06\_NEW\_COMB.pep.\*  
3: /cgn2\_6/prodata/2/paa/US07\_NEW\_COMB.pep.\*  
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7: /cgn2\_6/prodata/2/paa/US11\_NEW\_COMB.pep.\*  
8: /cgn2\_6/prodata/2/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2958	100.0	538	1	PCT-US03-28361-82
2	2958	100.0	538	1	PCT-US05-17514-6
3	2958	100.0	538	7	US-11-132-947-6
4	2958	100.0	547	6	US-10-940-774A-11544
5	1735.5	58.7	529	1	PCT-US05-17514-8
6	1735.5	58.7	529	7	US-11-132-947-8
7	1302	44.0	384	1	PCT-US05-07590-32
8	1302	44.0	384	7	US-11-075-351-32
9	278	9.4	551	1	PCT-US03-10870-439
10	278	9.4	551	7	US-11-033-545-308
11	278	9.4	551	8	US-60-685-372-1266
12	278	9.4	594	7	US-11-033-545-537
13	256	8.7	525	7	US-11-021-951-151
14	231	7.8	536	6	US-10-940-774A-8560
15	219.5	7.4	823	1	PCT-US04-17028-11
16	216	7.3	508	5	US-09-016-159D-7
17	215.5	7.3	521	1	PCT-US05-12464-58
18	215.5	7.3	521	7	US-11-105-268-58
19	215	7.3	522	6	US-10-412-703B-126
20	215	7.3	522	6	US-10-940-774A-6185
21	214	7.2	533	6	US-10-940-774A-9753
22	213	7.2	508	5	US-09-016-159D-5
23	211.5	7.2	896	1	PCT-US04-42360-2373
24	206	7.0	897	1	PCT-US05-15207-2184
25	206	7.0	897	8	US-60-685-372-1262

26	202.5	6.8	818	1	PCT-US04-17028-10	Sequence 10, Appl
27	193.5	6.5	825	1	PCT-US05-02350-130	Sequence 130, Appl
28	193.5	6.5	825	1	PCT-US04-17028-14	Sequence 14, Appl
29	193.5	6.5	825	6	US-10-287-436A-385	Sequence 385, Appl
30	193.5	6.5	825	6	US-10-287-436A-390	Sequence 390, Appl
31	193.5	6.5	825	6	US-10-287-436A-1085	Sequence 1085, Appl
32	193.5	6.5	825	6	US-10-287-436A-1090	Sequence 1090, Appl
33	193.5	6.5	825	7	US-11-043-770-130	Sequence 130, Appl
34	177	6.0	379	7	US-11-052-527-8	Sequence 8, Appl
35	177	6.0	379	7	US-11-052-527-8	Sequence 8, Appl
36	176	5.9	371	7	US-11-052-527-5	Sequence 5, Appl
37	176	5.9	371	7	US-11-052-527-5	Sequence 5, Appl
38	170	5.7	809	1	PCT-US04-17028-2	Sequence 2, Appl
39	170	5.7	809	1	PCT-US04-17028-15	Sequence 15, Appl
40	168.5	5.7	635	1	PCT-US05-15207-1589	Sequence 1589, Appl
41	168	5.7	369	7	US-11-052-527-12	Sequence 12, Appl
42	168	5.7	369	7	US-11-052-527-12	Sequence 12, Appl
43	162.5	5.5	223	1	PCT-US04-17028-9	Sequence 9, Appl
44	162.5	5.5	223	1	PCT-US04-17028-18	Sequence 18, Appl
45	162.5	5.5	357	7	US-11-052-527-9	Sequence 9, Appl

#### ALIGNMENTS

##### RESULT 1

PCT-US03-28361-82  
; Sequence 82, Application PC/TUS0328361  
; GENERAL INFORMATION:  
; APPLICANT: GENENTECH, INC.  
; APPLICANT: SARAH C. BODARY  
; APPLICANT: HILARY CLARK  
; APPLICANT: BRISDELL HUNTE  
; APPLICANT: JANET K. JACKMAN  
; APPLICANT: JILL SCHOENFELD  
; APPLICANT: P. MICKEY WILLIAMS  
; APPLICANT: WILLIAM I. WOOD  
; APPLICANT: THOMAS D. WU  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE  
; FILE REFERENCE: P1975R1-PCT  
; CURRENT APPLICATION NUMBER: PCT/US03/28361  
; CURRENT FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: US 60/410,174  
; PRIOR FILING DATE: 2002-09-11  
; NUMBER OF SEQ ID NOS: 104  
; SEQ ID NO 82  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US03-28361-82

Query Match 100.0%; Score 2958; DB 1; Length 538;  
Best Local Similarity 100.0%; Pred. No. 4.1e-201; Indels 0; Gaps 0;  
Matches 538; Conservative 0; Mismatches 0;

QY	1	MPRGWAAPLLILLQGWGCPDVCYTYLQTVICILEMNLHPSTLTITWDOYEEKLD 60	
DB	1	MPRGWAAPLLILLQGWGCPDVCYTYLQTVICILEMNLHPSTLTITWDOYEEKLD 60	
QY	61	EATSCSLHRSNAHNAHTATYTCMDVHFHMADDFSVNITDQSGNYSQECGSPFLAESIKP 120	
DB	61	EATSCSLHRSNAHNAHTATYTCMDVHFHMADDFSVNITDQSGNYSQECGSPFLAESIKP 120	
QY	121	APPENVTTFSGOYNISHRSDYEDPAFYMLKGKLOYELQYRNRGDPWAVSPRKLISVDS 180	
DB	121	APPENVTTFSGOYNISHRSDYEDPAFYMLKGKLOYELQYRNRGDPWAVSPRKLISVDS 180	
QY	181	RSVSLPPLLEFRKSDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEBELKEGWNPHLLL 240	
DB	181	RSVSLPPLLEFRKSDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEBELKEGWNPHLLL 240	
QY	241	LLLLLVIFIPAFWSLTKTHPLRWLWKKIWAVPSPERFFMPLYKGCSDGDFKWWGAPFTGSS 300	

Db 241 LLLLVIVIPAFWSLKTHTPLWRLWKIWAIVSPERFPMPLYKGCSDGFKKWGAPFTGSS 300  
QY 301 LELGWSPEVSTLEVYCHPPRSPAKRLQLTLOEPAELVESDGVKPKSPFWPTAQNSSG 360  
Db 301 LELGWSPEVSTLEVYCHPPRSPAKRLQLTLOEPAELVESDGVKPKSPFWPTAQNSSG 360  
QY 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSDGYPALDLDAGLESPGLEDPILD 420  
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSDGYPALDLDAGLESPGLEDPILD 420  
QY 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
Db 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
QY 481 PLAGLDMDTFDSGFGVSDCSPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGPQAS 538  
Db 481 PLAGLDMDTFDSGFGVSDCSPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGPQAS 538  
RESULT 2  
PCT-US05-17514-6  
; Sequence 6, Application PC/TUS0517514  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Kaesian, Marion  
; APPLICANT: Wood, Nancy L.  
; APPLICANT: Donaldson, Debra D.  
; TITLE OF INVENTION: MODULATION OF IMMUNOGLOBULIN PRODUCTION AND ATOPIC DISORDERS  
; FILE REFERENCE: 16158-016W01  
; CURRENT FILING DATE: 2005-05-24  
; PRIOR APPLICATION NUMBER: US 60/572,407  
; PRIOR FILING DATE: 2004-05-19  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US05-17514-6  
Query Match 100.0%; Score 2958; DB 1; Length 538;  
Best Local Similarity 100.0%; Pred. No. 4.1e-201;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MPRGWAAPLLLLLLQGGWGPCDLYCYTDYLTQTVICILEMMNLHPSTLTTLTWQDOYEELKD 60  
Db 1 MPRGWAAPLLLLLLQGGWGPCDLYCYTDYLTQTVICILEMMNLHPSTLTTLTWQDOYEELKD 60  
QY 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQRCGFLLAESIKP 120  
Db 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQRCGFLLAESIKP 120  
QY 121 APPENVTTFSGQYNIWSRSDYEDPAFYMLKGKLYLOEYLRNRPDPAVSPRRKLIISVDS 180  
Db 121 APPENVTTFSGQYNIWSRSDYEDPAFYMLKGKLYLOEYLRNRPDPAVSPRRKLIISVDS 180  
QY 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVI FQTQSEELKEGWNPHLLL 240  
Db 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVI FQTQSEELKEGWNPHLLL 240  
QY 241 LLLLVIVIPAFWSLKTHTPLWRLWKIWAIVSPERFPMPLYKGCSDGFKKWGAPFTGSS 300  
Db 241 LLLLVIVIPAFWSLKTHTPLWRLWKIWAIVSPERFPMPLYKGCSDGFKKWGAPFTGSS 300  
QY 301 LELGWSPEVSTLEVYCHPPRSPAKRLQLTLOEPAELVESDGVKPKSPFWPTAQNSSG 360  
Db 301 LELGWSPEVSTLEVYCHPPRSPAKRLQLTLOEPAELVESDGVKPKSPFWPTAQNSSG 360  
QY 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSDGYPALDLDAGLESPGLEDPILD 420  
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSDGYPALDLDAGLESPGLEDPILD 420  
QY 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
Db 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
QY 481 PLAGLDMDTFDSGFGVSDCSPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGPQAS 538  
Db 481 PLAGLDMDTFDSGFGVSDCSPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGPQAS 538

Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSDGYPALDLDAGLESPGLEDPILD 420  
QY 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
Db 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
QY 481 PLAGLDMDTFDSGFGVSDCSPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGPQAS 538  
Db 481 PLAGLDMDTFDSGFGVSDCSPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGPQAS 538  
RESULT 3  
US-11-132-947-6  
; Sequence 6, Application US/11132947  
; GENERAL INFORMATION:  
; APPLICANT: Kaesian, Marion  
; APPLICANT: Wood, Nancy L.  
; APPLICANT: Donaldson, Debra D.  
; APPLICANT: Collins, Mary  
; TITLE OF INVENTION: MODULATION OF IMMUNOGLOBULIN PRODUCTION AND ATOPIC DISORDERS  
; FILE REFERENCE: 16158-016001  
; CURRENT APPLICATION NUMBER: US/11/132,947  
; CURRENT FILING DATE: 2005-05-19  
; PRIOR APPLICATION NUMBER: US 60/572,407  
; PRIOR FILING DATE: 2004-05-19  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-132-947-6  
Query Match 100.0%; Score 2958; DB 7; Length 538;  
Best Local Similarity 100.0%; Pred. No. 4.1e-201;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MPRGWAAPLLLLLLQGGWGPCDLYCYTDYLTQTVICILEMMNLHPSTLTTLTWQDOYEELKD 60  
Db 1 MPRGWAAPLLLLLLQGGWGPCDLYCYTDYLTQTVICILEMMNLHPSTLTTLTWQDOYEELKD 60  
QY 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQRCGFLLAESIKP 120  
Db 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQRCGFLLAESIKP 120  
QY 121 APPENVTTFSGQYNIWSRSDYEDPAFYMLKGKLYLOEYLRNRPDPAVSPRRKLIISVDS 180  
Db 121 APPENVTTFSGQYNIWSRSDYEDPAFYMLKGKLYLOEYLRNRPDPAVSPRRKLIISVDS 180  
QY 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVI FQTQSEELKEGWNPHLLL 240  
Db 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVI FQTQSEELKEGWNPHLLL 240  
QY 241 LLLLVIVIPAFWSLKTHTPLWRLWKIWAIVSPERFPMPLYKGCSDGFKKWGAPFTGSS 300  
Db 241 LLLLVIVIPAFWSLKTHTPLWRLWKIWAIVSPERFPMPLYKGCSDGFKKWGAPFTGSS 300  
QY 301 LELGWSPEVSTLEVYCHPPRSPAKRLQLTLOEPAELVESDGVKPKSPFWPTAQNSSG 360  
Db 301 LELGWSPEVSTLEVYCHPPRSPAKRLQLTLOEPAELVESDGVKPKSPFWPTAQNSSG 360  
QY 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSDGYPALDLDAGLESPGLEDPILD 420  
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSDGYPALDLDAGLESPGLEDPILD 420  
QY 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
Db 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
QY 481 PLAGLDMDTFDSGFGVSDCSPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGPQAS 538  
Db 481 PLAGLDMDTFDSGFGVSDCSPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGPQAS 538



RESULT 4  
US-10-940-774A-11544  
; Sequence 11544, Application US/10940774A  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/10/940,774A  
; CURRENT FILING DATE: 2004-09-15  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11544  
; LENGTH: 547  
; TYPE: PRT  
; ORGANISM: Human  
US-10-940-774A-11544

Query Match 100.0%; Score 2958; DB 6; Length 547;  
Best Local Similarity 100.0%; Pred. No. 4.2e-201;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYQVVICILEMNNLHPSTLTWTQDQVEELKD 60  
DB 10 MPRGWAAPLLLLLQGGGCPDLVCYTDYQVVICILEMNNLHPSTLTWTQDQVEELKD 69  
  
QY 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSNNITDQSGNYSQCGSFLLAESIKP 120  
DB 70 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSNNITDQSGNYSQCGSFLLAESIKP 129  
  
QY 121 APPFNVTTFSGQYINISWRSDYEDPAFMYLKGKLYQYLRNGDPWAVSPRKLISVDS 180  
DB 130 APPFNVTTFSGQYINISWRSDYEDPAFMYLKGKLYQYLRNGDPWAVSPRKLISVDS 189  
  
QY 181 RSVLLPLEFRKDSYELQVRAGPMGSSYQGTWSESDPVIQTQSEBELKEGWNPHLL 240  
DB 190 RSVLLPLEFRKDSYELQVRAGPMGSSYQGTWSESDPVIQTQSEBELKEGWNPHLL 249  
  
QY 241 LLLLVIPIPAFWSLTKHPLRLWKKIWAIVFSPERFPMPLYKGCSDGFKWVGAPFTGSS 300  
DB 250 LLLLVIPIPAFWSLTKHPLRLWKKIWAIVFSPERFPMPLYKGCSDGFKWVGAPFTGSS 309  
  
QY 301 LELGWSPEVSTLEVYCHPPRSPAKRLQTLTEQPAELVESDGVKPSGVSSEAGS 360  
DB 310 LELGWSPEVSTLEVYCHPPRSPAKRLQTLTEQPAELVESDGVKPSGVSSEAGS 369  
  
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGCTWPCSCDDGYPALDLDAGLEPSGLEDPLD 420  
DB 370 SAYSEERDRPYGLVSDITVTVLDAEGCTWPCSCDDGYPALDLDAGLEPSGLEDPLD 429  
  
QY 421 AGTTVLSGCVSAGSAGSLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGVSSEAGS 480  
DB 430 AGTTVLSGCVSAGSAGSLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGVSSEAGS 489  
  
QY 481 FLAGLMDTDFSGFVSGSDCSFVCECDTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538  
DB 490 FLAGLMDTDFSGFVSGSDCSFVCECDTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 547

RESULT 5  
PCT-US05-17514-8  
; Sequence 8, Application PC/TUS0517514  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Kasaian, Marion  
; APPLICANT: Wood, Nancy L.

; APPLICANT: Donaldson, Debra D.  
; APPLICANT: Collins, Mary  
; TITLE OF INVENTION: MODULATION OF IMMUNOGLOBULIN PRODUCTION AND ATOPIC DISORDERS  
; FILE REFERENCE: 16158-016W01  
; CURRENT APPLICATION NUMBER: PCT/US05/17514  
; CURRENT FILING DATE: 2005-05-24  
; PRIOR APPLICATION NUMBER: US 60/572,407  
; PRIOR FILING DATE: 2004-05-19  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 8  
; LENGTH: 529  
; TYPE: PRT  
; ORGANISM: Mus musculus  
PCT-US05-17514-8

Query Match 58.7%; Score 1735.5; DB 1; Length 529;  
Best Local Similarity 62.7%; Pred. No. 1.2e-114;  
Matches 340; Conservative 49; Mismatches 136; Indels 17; Gaps 6;  
  
QY 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYQVVICILEMNNLHPSTLTWTQDQVEELKD 60  
DB 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYQVVICILEMNNLHPSTLTWTQDQVEELKD 60  
  
QY 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSNNITDQSGNYSQCGSFLLAESIKP 120  
DB 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSNNITDQSGNYSQCGSFLLAESIKP 120  
  
QY 121 APPFNVTTFSGQYINISWRSDYEDPAFMYLKGKLYQYLRNGDPWAVSPRKLISVDS 180  
DB 121 APPFNVTTFSGQYINISWRSDYEDPAFMYLKGKLYQYLRNGDPWAVSPRKLISVDS 180  
  
QY 181 RSVLLPLEFRKDSYELQVRAGPMGSSYQGTWSESDPVIQTQSEBELKEGWNPHLL 240  
DB 181 RSVLLPLEFRKDSYELQVRAGPMGSSYQGTWSESDPVIQTQSEBELKEGWNPHLL 240  
  
QY 241 LLLLVIPIPAFWSLTKHPLRLWKKIWAIVFSPERFPMPLYKGCSDGFKWVGAPFTGSS 299  
DB 241 LLAVALIIVL-VFMGLKHLPLRLWKKIWAIVTTPESFPQPLYREHSGNFKKWVNTPTAS 299  
  
QY 300 SLELGWSPEVSTLEVYCHPPRSPAKRLQTLTEQPAELVESDGVKPSFW---PTAQ 356  
DB 300 SLELGWSPEVSTLEVYCHPPRSPAKRLQTLTEQPAELVESDGVKPSFW---PTAQ 354  
  
QY 357 NSGSAYSEERDRPYGLVSDITVTVLDAEGCTWPCSCDDGYPALDLDAGLEPSGLED 416  
DB 355 QGAVSAYSEERDRPYGLVSDITVTVLDAEGCTWPCSCDDGYPALDLDAGLEPSGLED 414  
  
QY 417 PLLDAGTTVLSGCVSAGSAGSLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGVSSEAGS 476  
DB 415 LLLVTDPAFLSCGCVSGSLRGLGSGSLDLRLKPLADGEDWAGGLPWGGRSPGVSSEAGS 474  
  
QY 477 EAGSPLAGLMDTDFSGFVSGSDCSFVCECDTSPGDEGPPRSYLRQWVIPPPLSSPGQ 536  
DB 475 EAGSP-FGLDMDTDFSGFVSGSDCSFVCECDTSPGDEGPPRSYLRQWVIPPPLSSPGQ 527  
  
QY 537 AS 538  
DB 528 SS 529

RESULT 6  
US-11-132-947-8  
; Sequence 8, Application US/11132947  
; GENERAL INFORMATION:  
; APPLICANT: Kasaian, Marion  
; APPLICANT: Wood, Nancy L.  
; APPLICANT: Donaldson, Debra D.  
; APPLICANT: Collins, Mary  
; TITLE OF INVENTION: MODULATION OF IMMUNOGLOBULIN PRODUCTION AND ATOPIC DISORDERS  
; FILE REFERENCE: 16158-016001  
; CURRENT APPLICATION NUMBER: US/11/132,947  
; CURRENT FILING DATE: 2005-05-19

; PRIOR APPLICATION NUMBER: US 60/572,407  
; PRIOR FILING DATE: 2004-05-19  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 8  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-132-947-8

Query Match 58.7%; Score 1735.5; DB 7; Length 529;  
Best Local Similarity 62.7%; Pred. No. 1.2e-114;  
Matches 340; Conservative 49; Mismatches 136; Indels 17; Gaps 6;  
  
Qy 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVVICILEMNLHPSTLTLTWQDQYEELKD 60  
Db 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVVICILEMNLHPSTLTLTWQDQYEELKD 60  
  
Qy 61 EATCSLHRSAHNATHATYTCCHMDVHFHMADDIFSVNITDQSGNYSQECGFLAESAISKP 120  
Db 61 QETFCSLHRSAGHNTTHIWTCHMRLSQFLSDEVFVNVITDQSGNNSQECGFLAESAISKP 120  
  
Qy 121 APPENVTVTFSGQYNIWSRSDYEDPAFYMLKGKIQYELQYRNRGDPWAVSPRRKLISVDS 180  
Db 121 APPENVTVTFSGQYNIWSRSDYEDPAFYMLKGKIQYELQYRNRGDPWAVSPRRKLISVDS 180  
  
Qy 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237  
Db 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237  
  
Qy 241 LLLLVIVIPAFWSLKTPLRLMKKIWA-VPSPERFFMPLYKGCSDGDFKWKVGAFTGS 299  
Db 241 LLLLVIVIPAFWSLKTPLRLMKKIWA-VPSPERFFMPLYKGCSDGDFKWKVGAFTGS 299  
  
Qy 300 SLELGPWSPVPSTLEVYSCHPSPAKRLQTELQEPALVESDGVKPKSPFW---PTAQ 356  
Db 300 SLELGPWSPVPSTLEVYSCHPSPAKRLQTELQEPALVESDGVKPKSPFW---PTAQ 356  
  
Qy 357 NSGGSAYSEERDRPGLVSDITVTLDAEGPCTWPCSCDDGYPALDLDALESPGLED 416  
Db 357 NSGGSAYSEERDRPGLVSDITVTLDAEGPCTWPCSCDDGYPALDLDALESPGLED 416  
  
Qy 417 PLLDAGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSES 476  
Db 417 PLLDAGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSES 476  
  
Qy 477 EAGSP-PLGLDMDTFDSGFGSDCSPVECDFTSPGDEGPPRSYLRQWVVIPIPLSSPGPQ 536  
Db 477 EAGSP-PLGLDMDTFDSGFGSDCSPVECDFTSPGDEGPPRSYLRQWVVIPIPLSSPGPQ 536  
  
Qy 537 AS 538  
Db 537 AS 538

RESULT 7  
PCT-US05-07590-32  
; Sequence 32, Application PC/TUS0507590  
; GENERAL INFORMATION:  
; APPLICANT: ZymoGenetics, Inc.  
; TITLE OF INVENTION: DIMERIC FUSION PROTEINS AND MATERIALS  
; FILE REFERENCE: 02-16PC  
; CURRENT APPLICATION NUMBER: PCT/US05/07590  
; CURRENT FILING DATE: 2005-03-08  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 32  
; LENGTH: 384  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: fusion protein

PCT-US05-07590-32

Query Match 44.0%; Score 1302; DB 1; Length 384;  
Best Local Similarity 100.0%; Pred. No. 3.6e-84;  
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVVICILEMNLHPSTLTLTWQDQYEELKD 60  
Db 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVVICILEMNLHPSTLTLTWQDQYEELKD 60  
  
Qy 61 EATCSLHRSAHNATHATYTCCHMDVHFHMADDIFSVNITDQSGNYSQECGFLAESAISKP 120  
Db 61 EATCSLHRSAHNATHATYTCCHMDVHFHMADDIFSVNITDQSGNYSQECGFLAESAISKP 120  
  
Qy 121 APPENVTVTFSGQYNIWSRSDYEDPAFYMLKGKIQYELQYRNRGDPWAVSPRRKLISVDS 180  
Db 121 APPENVTVTFSGQYNIWSRSDYEDPAFYMLKGKIQYELQYRNRGDPWAVSPRRKLISVDS 180  
  
Qy 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237  
Db 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237

RESULT 8  
US-11-075-351-32  
; Sequence 32, Application US/11075351  
; GENERAL INFORMATION:  
; APPLICANT: Moore, Margaret D.  
; TITLE OF INVENTION: DIMERIC FUSION PROTEINS AND MATERIALS  
; FILE REFERENCE: 02-16  
; CURRENT APPLICATION NUMBER: US/11/075,351  
; CURRENT FILING DATE: 2005-03-08  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 32  
; LENGTH: 384  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: fusion protein  
US-11-075-351-32

Query Match 44.0%; Score 1302; DB 7; Length 384;  
Best Local Similarity 100.0%; Pred. No. 3.6e-84;  
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVVICILEMNLHPSTLTLTWQDQYEELKD 60  
Db 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVVICILEMNLHPSTLTLTWQDQYEELKD 60  
  
Qy 61 EATCSLHRSAHNATHATYTCCHMDVHFHMADDIFSVNITDQSGNYSQECGFLAESAISKP 120  
Db 61 EATCSLHRSAHNATHATYTCCHMDVHFHMADDIFSVNITDQSGNYSQECGFLAESAISKP 120  
  
Qy 121 APPENVTVTFSGQYNIWSRSDYEDPAFYMLKGKIQYELQYRNRGDPWAVSPRRKLISVDS 180  
Db 121 APPENVTVTFSGQYNIWSRSDYEDPAFYMLKGKIQYELQYRNRGDPWAVSPRRKLISVDS 180  
  
Qy 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237  
Db 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237

RESULT 9  
PCT-US03-10870-439  
; Sequence 439, Application PC/TUS0310870  
; GENERAL INFORMATION:  
; APPLICANT: Mitokor, Inc.  
; APPLICANT: Buck Institute  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Faby, Eoin D.

```
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465PC
; CURRENT APPLICATION NUMBER: PCT/US03/10870
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3025
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 439
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-10870-439

Query Match          9.4%; Score 278; DB 1; Length 551;
Best Local Similarity 26.0%; Pred. No. 1.5e-11;
Matches 137; Conservative 75; Mismatches 199; Indels 116; Gaps 31;

QY 5 WAAPLILLL--LQGGW-----GCPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYE 56
DB 8 WRLPLLILLLPLATSWASAAVNGTSQFTCFYNSRANISCV---WS-----QDG 52

QY 57 ELKDEATSCSLH-----RSAHNAT-----HATYTCM-----DVHFMAADDIFSUNITD 100
DB 53 ALQD--TSCQVHAMPDRRRWNTCELLPVSAQSWACNLILGAPDSQKLTITVDIVTLRLVC 110

QY 101 QSGNYSQEGC--SPILLAESIKAPPNVTVP--SGQYNISWRSDYEDPAFVLMKGLQY 156
DB 111 REGVRWRYMAIQDFKPFENLRMAPISLQVVHVHETHRCNISWEI---SQASHYFERHLEF 167

QY 157 ELQYNRGDPWAVSPRRKLIISVDSRSVLLPLEFRKDSYELQVRAGMPGSSYQGTWSE 216
DB 168 EARTLSPGHTWEAP---LLTLKQEWICLETITPDQYEFQVRVKPLQGEF--TTWSP 222

QY 217 WSDPVIFQTSBELKEG---WNPHLLLLLLLVIFIPAFWSL-----KTHPLWRLW--KKIW 268
DB 223 WSQLAFRTKPAALGKDTIPWLGHLVGLSGAFGIILVYLLINCRNTGP---WLKKVL 278

QY 269 A--VSPERPFMPLYKGCSDFKKVGAPPTGSSLELGPWSPDEVSTLEVYSCHPPRSPA 326
DB 279 KCNTDPSPKFFSQLSSEHGSDVQKWLSPFPSSPFGGLAPEI--SPLEV-----L 328

QY 327 KRLQLTQLQEPALVELSDGVPKPSFWPTAONGSGSAYSEERDRPYGLVSIIDTVTLDAEG 386
DB 329 ERDKVTQL-----LQODKVPEPA-----SLSNHSLTSCFTNQGYFFPHLPDALEIEA-- 377

QY 387 PC-----TWPCSCDD-----GYPALDLDAGLESPGLEPDLDAAGTTVLSGCVSAGSP 436
DB 378 -CQVYFTYDPYSEEDPDEGVAGAPTSSPQPLQPSG-ED---DAYCTFPSPRDDLLLSF 432

QY 437 G-LGSP-----LGSLLDRLKPLAD--GEDWAGGLPWGGRSPG 471
DB 433 SLLGSPSPSTAPGSGAGEERMPESLQERVPRDW-DPQPLGPPTPG 478

RESULT 10
US-11-033-545-308
; Sequence 308, Application US/11033545
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/11/033,545
; CURRENT FILING DATE: 2005-01-12
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 308
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Human
US-11-033-545-308

Query Match          9.4%; Score 278; DB 7; Length 551;
Best Local Similarity 26.0%; Pred. No. 1.5e-11;
Matches 137; Conservative 75; Mismatches 199; Indels 116; Gaps 31;

QY 5 WAAPLILLL--LQGGW-----GCPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYE 56
DB 8 WRLPLLILLLPLATSWASAAVNGTSQFTCFYNSRANISCV---WS-----QDG 52

QY 57 ELKDEATSCSLH-----RSAHNAT-----HATYTCM-----DVHFMAADDIFSUNITD 100
DB 53 ALQD--TSCQVHAMPDRRRWNTCELLPVSAQSWACNLILGAPDSQKLTITVDIVTLRLVC 110

QY 101 QSGNYSQEGC--SPILLAESIKAPPNVTVP--SGQYNISWRSDYEDPAFVLMKGLQY 156
DB 111 REGVRWRYMAIQDFKPFENLRMAPISLQVVHVHETHRCNISWEI---SQASHYFERHLEF 167

QY 157 ELQYNRGDPWAVSPRRKLIISVDSRSVLLPLEFRKDSYELQVRAGMPGSSYQGTWSE 216
DB 168 EARTLSPGHTWEAP---LLTLKQEWICLETITPDQYEFQVRVKPLQGEF--TTWSP 222

QY 217 WSDPVIFQTSBELKEG---WNPHLLLLLLLVIFIPAFWSL-----KTHPLWRLW--KKIW 268
DB 223 WSQLAFRTKPAALGKDTIPWLGHLVGLSGAFGIILVYLLINCRNTGP---WLKKVL 278

QY 269 A--VSPERPFMPLYKGCSDFKKVGAPPTGSSLELGPWSPDEVSTLEVYSCHPPRSPA 326
DB 279 KCNTDPSPKFFSQLSSEHGSDVQKWLSPFPSSPFGGLAPEI--SPLEV-----L 328

QY 327 KRLQLTQLQEPALVELSDGVPKPSFWPTAONGSGSAYSEERDRPYGLVSIIDTVTLDAEG 386
DB 329 ERDKVTQL-----LQODKVPEPA-----SLSNHSLTSCFTNQGYFFPHLPDALEIEA-- 377

QY 387 PC-----TWPCSCDD-----GYPALDLDAGLESPGLEPDLDAAGTTVLSGCVSAGSP 436
DB 378 -CQVYFTYDPYSEEDPDEGVAGAPTSSPQPLQPSG-ED---DAYCTFPSPRDDLLLSF 432

QY 437 G-LGSP-----LGSLLDRLKPLAD--GEDWAGGLPWGGRSPG 471
DB 433 SLLGSPSPSTAPGSGAGEERMPESLQERVPRDW-DPQPLGPPTPG 478

RESULT 11
US-60-685-372-1266
; Sequence 1266, Application US/60685372
; GENERAL INFORMATION:
; APPLICANT: Belouchi, Abdelmajid
; APPLICANT: Raelson, John V
; APPLICANT: Bradley, Walter E
; APPLICANT: Paquin, Bruno
; APPLICANT: Nguyen-Huu, Quynh
; APPLICANT: Croteau, Pascal
; APPLICANT: Allard, Rene
; APPLICANT: Little, Randall D
; APPLICANT: Cousineau, Johanne
; APPLICANT: Eerdewegh, Paul V
; APPLICANT: Segal, Jonathan
; TITLE OF INVENTION: GeneMap of the Human Genes Associated with Psoriasis
; FILE REFERENCE: 059908-5005-PR
; CURRENT APPLICATION NUMBER: US/60/685,372
; CURRENT FILING DATE: 2005-05-31
; NUMBER OF SEQ ID NOS: 2738
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1266
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-60-685-372-1266

Query Match 9.4%; Score 278; DB 8; Length 551;

Best Local Similarity 26.0%; Pred. No. 1.5e-11;

Matches 137; Conservative 75; Mismatches 199; Indels 116; Gaps 31;

QY 5 WAAPLLILL--LQGGW-----GCPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYE 56

DB 8 WRLPLLILLPLATWSAAVNGTSQFTCFYNSRANISCV---WS-----QDG 52

QY 57 ELKDEATSCSLH-----RSAHNA-----HATYTCM-----DVHFMAADIFSVNITD 100

DB 53 ALQD--TSCQVHAWPDRRRWNTQCELLPVSQASWACNLILGAPDSQKLTITVDIVTLRVLC 110

QY 101 QSGNYSQEG--SPLLAESIKPAPPFNVTYTF--SGQYNISWRSDYEDPAPFVLMKGLQY 156

DB 111 REGVRWVMAIQDFKPFENLRMAPISLQVHVHETHRCNISWEI---SQASHYFERHLEF 167

QY 157 ELQVRNRGDPWAVSPRRKLISVDRSVSLLLPLEFRKDSYSELQVRAGMPGSSYQGTWSE 216

DB 168 EARTLSFGHTWEEAP---LLTLKQKQEWICLETTLTPDTQYEFQVRVKPLOGEF--TTWSP 222

QY 217 WSDPVIFQTSSEELKEG---WNPHLLLLLLVIVIPAFWSL-----KTHPLWRLW-KKIW 268

DB 223 WSQPLAFRTKPAALGKDTIPMLGHLVGLSGAFGIILVYLLINCRNTGP-----WLKKVL 278

QY 269 A--VPSPERFMPYKGCSDGFKKWGAPFTGSSLELGPWSPVSTLEVYVCHPPRSPA 326

DB 279 KCNTPDPSKFPSSSEHGDDVQKWLSSPSSPSSPGLAPEI--SPLEV-----L 328

QY 327 KRLQLTEQPAELVESDGVKPSFWPTAQNSGGSAYSEERDRPYGLVSIIDTVTLDAEG 386

DB 329 ERDKVTQL-----LQQDKVPEPA-----SLSNHSLTSCFTNQGYFFPHLPDALEIEA-- 377

QY 387 PC-----TWPSCEDD-----GYPALDLDAGLESPGLEPDLDDAGTTVLSCGCVSAGSP 436

DB 378 -CQVYFTYDPYSEEDPDEGVAGAPTGSSPQPLQPLSG-ED---DAYCTFSPRDDLLLFSP 432

QY 437 G-LGGP-----LGSLLDLRLKPLAD--GEDWAGGLPWGGRSPG 471

DB 433 SLLGGPSPSTAPGGSGAGEERMPPSLQERVRDWM-DPQPLGPPTPG 478

RESULT 12

US-11-033-545-537

; Sequence 537, Application US/11033545

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: CL000790

; CURRENT APPLICATION NUMBER: US/11/033,545

; CURRENT FILING DATE: 2005-01-12

; PRIOR APPLICATION NUMBER: 60/231,401

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 10823

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 537

; LENGTH: 594

; TYPE: PRT

; ORGANISM: Human

US-11-033-545-537

Query Match 9.4%; Score 278; DB 7; Length 594;

Best Local Similarity 26.0%; Pred. No. 1.6e-11;

Matches 137; Conservative 75; Mismatches 199; Indels 116; Gaps 31;

QY 5 WAAPLLILL--LQGGW-----GCPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYE 56

DB 51 WRLPLLILLPLATWSAAVNGTSQFTCFYNSRANISCV---WS-----QDG 95

QY 57 ELKDEATSCSLH-----RSAHNA-----HATYTCM-----DVHFMAADIFSVNITD 100

DB 96 ALQD--TSCQVHAWPDRRRWNTQCELLPVSQASWACNLILGAPDSQKLTITVDIVTLRVLC 153

QY 101 QSGNYSQEG--SPLLAESIKPAPPFNVTYTF--SGQYNISWRSDYEDPAPFVLMKGLQY 156

DB 154 REGVRWVMAIQDFKPFENLRMAPISLQVHVHETHRCNISWEI---SQASHYFERHLEF 210

QY 157 ELQVRNRGDPWAVSPRRKLISVDRSVSLLLPLEFRKDSYSELQVRAGMPGSSYQGTWSE 216

DB 211 EARTLSFGHTWEEAP---LLTLKQKQEWICLETTLTPDTQYEFQVRVKPLOGEF--TTWSP 265

QY 217 WSDPVIFQTSSEELKEG---WNPHLLLLLLVIVIPAFWSL-----KTHPLWRLW-KKIW 268

DB 266 WSQPLAFRTKPAALGKDTIPMLGHLVGLSGAFGIILVYLLINCRNTGP-----WLKKVL 321

QY 269 A--VPSPERFMPYKGCSDGFKKWGAPFTGSSLELGPWSPVSTLEVYVCHPPRSPA 326

DB 322 KCNTPDPSKFPSSSEHGDDVQKWLSSPSSPSSPGLAPEI--SPLEV-----L 371

QY 327 KRLQLTEQPAELVESDGVKPSFWPTAQNSGGSAYSEERDRPYGLVSIIDTVTLDAEG 386

DB 372 ERDKVTQL-----LQQDKVPEPA-----SLSNHSLTSCFTNQGYFFPHLPDALEIEA-- 420

QY 387 PC-----TWPSCEDD-----GYPALDLDAGLESPGLEPDLDDAGTTVLSCGCVSAGSP 436

DB 421 -CQVYFTYDPYSEEDPDEGVAGAPTGSSPQPLQPLSG-ED---DAYCTFSPRDDLLLFSP 475

QY 437 G-LGGP-----LGSLLDLRLKPLAD--GEDWAGGLPWGGRSPG 471

DB 476 SLLGGPSPSTAPGGSGAGEERMPPSLQERVRDWM-DPQPLGPPTPG 521

RESULT 13

US-11-021-951-151

; Sequence 151, Application US/11021951

; GENERAL INFORMATION:

; APPLICANT: HAUPTS, Ulrich

; APPLICANT: SCHEIDIG, Andreas

; APPLICANT: VOTSMEIER, Christian

; APPLICANT: Kettling, Ulrich

; APPLICANT: COCO, Wayne Michael

; TITLE OF INVENTION: New Biological Entities And The Pharmaceutical

; TITLE OF INVENTION: And Diagnostic Use Thereof

; FILE REFERENCE: 04156.0002U5

; CURRENT APPLICATION NUMBER: US/11/021,951

; CURRENT FILING DATE: 2004-12-22

; PRIOR APPLICATION NUMBER: 10/872,198

; PRIOR FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: 60/543,518

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: 60/524,960

; PRIOR FILING DATE: 2003-11-25

; PRIOR APPLICATION NUMBER: EP 040003058

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: EP 03025871

; PRIOR FILING DATE: 2003-11-11

; PRIOR APPLICATION NUMBER: EP 03025851

; PRIOR FILING DATE: 2003-11-10

; PRIOR APPLICATION NUMBER: EP 03013819

; PRIOR FILING DATE: 2003-06-18

; NUMBER OF SEQ ID NOS: 191

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 151

; LENGTH: 525

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-021-951-151

Query Match 8.7%; Score 256; DB 7; Length 525;

Best Local Similarity 25.5%; Pred. No. 5e-10;

Matches 129; Conservative 74; Mismatches 194; Indels 108; Gaps 29;

QY 19 GCPDLVCYDYLTQVTCILEMNLHPSTLTLTWQDQYEEKDEATSCSLH-----BSAHNA 74  
Db 4 GTSQFTCFYNSRANISCV---WS-----ODGALQD--TSCQVHAMDPDRRRMNQ 46  
QY 75 T-----HATYTCM-----DVHFPMADDIFSUNITQSGNYSQECG--SFLLAESIKP 120  
Db 47 TCELLPVQSQASMACNLLIGAPDSQKLTVDIVTLVLCREGVVRWMAIQDFKPFENLRL 106  
QY 121 APPFNVTTF--SGQYNISWRSDYEDPAFMYLKGKQYELQYLRNRGDPMAVSPRKLISV 178  
Db 107 MAPISLQVHVHETHRCNISWEI---SQASHYFERHLEFEARTLSPGHTWEEAP---LLTL 160  
QY 179 DRSVSLLPLERKSSYELQYLRAGMPGSSVQGTWSESDPVIPTQOSEELKEG---WN 235  
Db 161 KQKQEMICLETPTDQYEFQVRVPLQGEF--TTWSPMSQPLAFKTPAALGKOTIPML 218  
QY 236 PHLLLLLLVIVIFAFWSL-----KTHPLRLW--KKIWA--VPSPERFFMPLYKGCSDG 288  
Db 219 GHLVCLSGAFGFIILVILLINCRNTGP-----WLKVKLCNTPDPSKFSQLSSEHGSDV 274  
QY 289 KKWVGAPFTGSSLELGPMSPEVPSTLEVYCHPPRSPAKRLQTELQEPALVESDGVPK 348  
Db 275 QKWLSPPSPSSFSFGGLAPEI--SPLEV-----LERDKVTQL-----LLQDDKVPE 319  
QY 349 PSFWPTAONGSGSAYSEERDRPYGLVSDTVTVLDAEGPC-----TWPCSCDD-----G 398  
Db 320 PA-----SUSNHSLSCTFNOGYFFPHFLPDALIEIA--CQYFYDYPSSEDDPDGVAG 372  
QY 399 YPALDLDALESPGLEPDLDTAGTTLSCGCVSAGSPG--LGPP-----LGSLLDR 448  
Db 373 ATGSSPQLPLSG--ED---DAYCTFPRDRDILLFSPSLGPGPPPTAPGSGAGBER 428  
QY 449 LKPPILAD--GEDWAGGLPWGRSPG 471  
Db 429 MPESLQERVRDW--DQPLGPPTEG 452

RESULT 14  
US-10-940-774A-8560  
; Sequence 8560, Application US/10940774A  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/10/940,774A  
; CURRENT FILING DATE: 2004-09-15  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8560  
; LENGTH: 536  
; TYPE: PRT  
; ORGANISM: Human  
US-10-940-774A-8560

Query Match 7.8%; Score 231; DB 6; Length 536;  
Best Local Similarity 25.2%; Pred. No. 3e-08;  
Matches 143; Conservative 53; Mismatches 206; Indels 166; Gaps 34;

QY 17 GNGCPDLVCYDYLTQVTCILEMNLHPSTLTLTWQDQYEEKDEATSC-----65  
Db 8 GNGCLRLV-----MGLGRCIWEGTWLESEALRDMGTW-----LLACICICTVCV 52  
QY 66 ----SLHRSAHNATHATYTC-----HMDVFHFMADD-----IFSVNITDQSGNY-- 105  
Db 53 LGVSVTGEQGRSRRTFTCLTNILRIDC--HWSAPELGGSSPFWLLFTSN--QAPGTHKC 110

QY 106 ---SOECGSFLLAESIKPAPPFNVTTF-----SGQYNISW-----RSDYE 143  
Db 111 ILRGSECTVLPPEAVL--VPSDNFTITTHCMCSGREGVSLVDPBYLPRRHVKLDPPSDIQ 169  
QY 144 -----DPAFMYLKGKQYELQYLRNRGDPMAVSPRKLISVDRSRVSLPLLE 189  
Db 170 SNISGHCILLTWSISPALPEPMTLLSYELAFKKQEEAMEQAHRDHIV-----GVTWLLILE 225  
QY 190 -FRKDSY-----ELQVRAGMPG-----SSYQGTWSESDPVIPTQOSEE-----LKEGWN 235  
Db 226 AFELDPGFIHEARLRVQMATLEDDVVEBERYTQGWSEWSQVCFQAPQOQGLIPPWGWP 285  
QY 236 PHLLLLLLVIVIFAFWSLATHPLRLW-----KKIWA--AVPSPERFFMPLYKGCSD 287  
Db 286 GN---TLVAVSIFL-----LUTGPTYLLFLKLSPRVKRIFYQNVPSPAFFQBLYSVHNG 337  
QY 288 FKKWVGAPFTGSSLE-----LGPMSPEVPSTLEVYCHPPRSPAKRLQTELQE-----336  
Db 338 FQTMGAHAGAGVILLSQDCAGTFQGNALFCVQEAETALLTCGPAP--PWKSVALEEEGEGPCT 396  
QY 337 --PAELVESDGVKPSFWMPTAONGSGSAYSEERDRPYGLVSDTVTVLDAEG--PCTWPC 392  
Db 397 RLPGNLSSEDDVLPAGC---TEWRVQTLAYLPQED--WAPTSLTRPAPPDSEGRSSSSSS 451  
QY 333 SCEDDGYPALDLDAEG--LEPSPGLE-----PLLDAGTTLVLS-----CCVSAG 434  
Db 452 SSNNNYCALGCGYGGHLSALPGNTQSSGPIPALACG---LSCDHQGLETOQGVAVMLAG 508  
QY 435 ---SPGLGGLGSLDLRLKPLADGEDW 459  
Db 509 HCQRPGLHEDLQGLM--LPSVLKXRSW 534

Query Match 7.4%; Score 219.5; DB 1; Length 823;  
Best Local Similarity 22.3%; Pred. No. 3.4e-07;  
Matches 142; Conservative 67; Mismatches 221; Indels 207; Gaps 35;

QY 17 GNGCPDLV-----CYTDYLTQVTCILEMNL--HPST-----L 47  
Db 2 GMLCSGLTFPVSCVLVWVASSGSKVHLHFCFSFYISTSVCS---QMKMDHPTNCSAEL 58  
QY 48 TLTWQDQYEEKDEATSCSLHRSAHNATHATYTCMVFHFMADDIFSUNITDQSGNSQ 107  
Db 59 RLSYQLDF--MGSENHTC---VPENRREDSVCVCSMPIDDAVEADYQDL--WAGQQL 110  
QY 108 ECGSFLLAESIKPAPPFNVTV--TFSGQYNISWRSDYEDPAFMYLKGKQYELQYLRNRGD 165  
Db 111 WSGSPQSKVKRPTFGNLTVHPNISHTWLLMTNTPY--PTENHLHSELTYMVNVNSND 168

RESULT 15  
PCT-US04-17028-11  
; Sequence 11, Application PC/TUS0417028  
; GENERAL INFORMATION:  
; APPLICANT: Watson, Johanna L.  
; APPLICANT: Jackson, Kenneth A.  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: IL4 Receptor Antagonists for Horse, Dog and Cat  
; FILE REFERENCE: 023070-133820PC  
; CURRENT APPLICATION NUMBER: PCT/US04/17028  
; CURRENT FILING DATE: 2004-05-28  
; PRIOR APPLICATION NUMBER: US 60/475,220  
; PRIOR FILING DATE: 2003-05-30  
; PRIOR APPLICATION NUMBER: US 60/561,579  
; PRIOR FILING DATE: 2004-04-12  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 823  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
; FEATURE:  
; OTHER INFORMATION: dog interleukin-4 (IL4) receptor (IL4R)  
PCT-US04-17028-11

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QY 166 PWAVSPRKLISVD--SRVSILLPLERKSSSYELOVRAGPMGSSYQGTWSEWSDPVP 223
Db 169 P-----EDFKVTNVTMGFTLRLAASSTLKSAGSYARVRW---AQTYNSTWSDNSP----- 217
QY 224 QTQSEELKEGWNPHLL-----LLLLVIVFIPAFWSLKTHTPLWRLMKKIWAVPSP----- 273
Db 218 STRMLNYYEPWEQHPLGVISLCLVLAICLCYFSIIKIKKGW--WDQI---ENPAHSP 272
QY 274 -----ERFMPLYKGC-----SGDFKKWVGAPPTGSSLEL 303
Db 273 LVAVIQDSQVSLWGKRSGQEPKCPHWKCTLTKLLPCLLEHGLGREESPKTKNGPL 332
QY 304 -GP-----WSP-EV-----PSTLEVYSCHPPRSPAKRLQLTEL---QEPALVESDGVPK 348
Db 333 QOPGKPAWCPVEVSKTILWPESISVVQC-----VELSEAPVDNEEEVEED---K 380
QY 349 PSFWPTAQNGSGSAYSEERDRPYGLVSIIDTVTV-LDAEGPCTWPCSCEDDGYPALDLDA 407
Db 381 RSLCFSLGSGGS-FQEGRE--GIVARLTESLFLDLGG-----ENGFCFCQGLEES 429
QY 408 LEPSGLEDPLLDAGTTVLSCGVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGG 467
Db 430 CLPPPS-----GSVGAQMPWAQFP-----RAGPRAA-----PEGP 459
QY 468 RSPGVSESEAGSPLAGLMDTF-----DSGFVGSDD---CS 500
Db 460 EQRRPESALQASPTQSAGSAFEPFPVTVTDNPAYSFGSFLGSSDPGSDPGLAD 519
QY 501 SPVECDFTSPGDEGPPRSYLRQWVVI PPPPLSPGQFA 537
Db 520 RPGEADPGIPSAQPPE-----PPAALQPRPES 547
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Search completed: July 9, 2005, 11:57:52  
Job time : 66 secs

GenCore version 5.1.16  
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OM protein - protein search, using sw model

Run on: July 9, 2005, 11:41:15 ; Search time 475 Seconds  
(without alignments)  
1322.921 Million cell updates/sec

Title: US-10-620-169-4

Perfect score: 2958

Sequence: 1 MPRGWAAPLLLLLLQLGGWGC.....YLRQWVIPPPLSSPGPOAS 538

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Pending Patents AA Main:\*
- 1: /cgn2\_6/ptodata/1/paa/PCTUS COMB.pcp.\*
  - 2: /cgn2\_6/ptodata/1/paa/US06 COMB.pcp.\*
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  - 25: /cgn2\_6/ptodata/1/paa/US099B COMB.pcp.\*
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  - 27: /cgn2\_6/ptodata/1/paa/US101 COMB.pcp.\*
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  - 34: /cgn2\_6/ptodata/1/paa/US108 COMB.pcp.\*
  - 35: /cgn2\_6/ptodata/1/paa/US109 COMB.pcp.\*
  - 36: /cgn2\_6/ptodata/1/paa/US110 COMB.pcp.\*
  - 37: /cgn2\_6/ptodata/1/paa/US60 COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2958	100.0	538	1	PCT-US00-06067-115	Sequence 115, Appl
2	2958	100.0	538	1	PCT-US00-13687-2	Sequence 2, Appli
3	2958	100.0	538	1	PCT-US02-29839-2	Sequence 2, Appli
4	2958	100.0	538	1	PCT-US02-34502-16	Sequence 16, Appl
5	2958	100.0	538	1	PCT-US03-17808-6	Sequence 6, Appli
6	2958	100.0	538	1	PCT-US03-21975-4	Sequence 4, Appli
7	2958	100.0	538	1	PCT-US04-08833-6	Sequence 6, Appli
8	2958	100.0	538	15	US-09-159-254-2	Sequence 2, Appli
9	2958	100.0	538	16	US-09-264-908-2	Sequence 2, Appli
10	2958	100.0	538	16	US-09-265-117-2	Sequence 2, Appli
11	2958	100.0	538	17	US-09-313-913-2	Sequence 2, Appli
12	2958	100.0	538	17	US-09-347-930-2	Sequence 2, Appli
13	2958	100.0	538	19	US-09-543-320-2	Sequence 2, Appli
14	2958	100.0	538	19	US-09-560-766-2	Sequence 2, Appli
15	2958	100.0	538	19	US-09-569-384-2	Sequence 2, Appli
16	2958	100.0	538	19	US-09-574-100-2	Sequence 2, Appli
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18	2958	100.0	538	21	US-09-720-285-7	Sequence 7, Appli
19	2958	100.0	538	25	US-09-965-313-2	Sequence 2, Appli
20	2958	100.0	538	25	US-09-972-218A-2	Sequence 2, Appli
21	2958	100.0	538	25	US-09-972-218B-2	Sequence 2, Appli
22	2958	100.0	538	27	US-10-170-205E-23124	Sequence 23124, A
23	2958	100.0	538	28	US-10-264-634-2	Sequence 2, Appli
24	2958	100.0	538	28	US-10-282-622-16	Sequence 16, Appl
25	2958	100.0	538	30	US-10-456-262A-6	Sequence 6, Appli
26	2958	100.0	538	30	US-10-456-780-6	Sequence 6, Appli
27	2958	100.0	538	32	US-10-620-169-4	Sequence 4, Appli
28	2958	100.0	538	32	US-10-659-684-115	Sequence 115, App
29	2958	100.0	538	33	US-10-715-998-2	Sequence 2, Appli
30	2958	100.0	538	33	US-10-787-442-115	Sequence 115, App
31	2958	100.0	538	33	US-10-798-380-43	Sequence 43, Appl
32	2958	100.0	538	34	US-10-806-611-6	Sequence 6, Appli
33	2958	100.0	538	34	US-10-864-249-2	Sequence 2, Appli
34	2958	100.0	538	34	US-10-872-087-2	Sequence 2, Appli
35	2958	100.0	538	35	US-10-951-239-10	Sequence 10, Appl
36	2958	100.0	538	37	US-60-453-050-9170	Sequence 9170, Ap
37	2958	100.0	538	37	US-60-453-135-9170	Sequence 4984, Ap
38	2958	100.0	538	37	US-60-455-444-4984	Sequence 4984, Ap
39	2958	100.0	538	37	US-60-455-241-4984	Sequence 4984, Ap
40	2958	100.0	538	37	US-60-466-412-9170	Sequence 9170, Ap
41	2958	100.0	538	37	US-60-505-919-10	Sequence 10, Appl
42	2958	100.0	547	35	US-10-940-774-11544	Sequence 11544, A
43	2951	99.8	538	1	PCT-US99-25617-2	Sequence 2, Appli
44	2951	99.8	538	15	US-09-187-711-2	Sequence 2, Appli
45	2951	99.8	538	15	US-09-187-711A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
PCT-US00-06067-115  
; Sequence 115, Application PC/TUS0006067  
; GENERAL INFORMATION:  
; APPLICANT: ZymoGenetics, Inc.  
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND  
; FILE REFERENCE: 99-16PC  
; CURRENT APPLICATION NUMBER: PCT/US00/06067  
; CURRENT FILING DATE: 2000-03-09  
; EARLIER APPLICATION NUMBER: US 09/264,908  
; EARLIER FILING DATE: 1999-03-09  
; EARLIER APPLICATION NUMBER: US 09/265,992  
; EARLIER FILING DATE: 1999-03-11  
; EARLIER APPLICATION NUMBER: US 60/142,013  
; EARLIER FILING DATE: 1999-07-01  
; NUMBER OF SEQ ID NOS: 115  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 115  
; LENGTH: 538



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; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-06067-115

Query Match      100.0%; Score 2958; DB 1; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-236;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGWAAPLLLLLLOGGCGCPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60
DB 1 MPRGWAAPLLLLLLOGGCGCPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60

QY 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120
DB 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120

QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLOYELOYNRNGDPWAVSPRRKLIISVDS 180
DB 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLOYELOYNRNGDPWAVSPRRKLIISVDS 180

QY 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240
DB 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240

QY 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120
DB 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120

QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLOYELOYNRNGDPWAVSPRRKLIISVDS 180
DB 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLOYELOYNRNGDPWAVSPRRKLIISVDS 180

QY 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240
DB 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240

QY 241 LLLLVIVIPAFWSLTKTHPLWRLWKIWA VSPERFFMPLYKGCSDGPKKWWGAPFTGSS 300
DB 241 LLLLVIVIPAFWSLTKTHPLWRLWKIWA VSPERFFMPLYKGCSDGPKKWWGAPFTGSS 300

QY 301 LELGWPSPVSTLEVYSCHPPRSPAKRLQLTELQEPAAELVESDGVKPKSPFWPTAQNSSG 360
DB 301 LELGWPSPVSTLEVYSCHPPRSPAKRLQLTELQEPAAELVESDGVKPKSPFWPTAQNSSG 360

QY 361 SAYSEERDRPYGLVSIIDTVTVLDAEGCTWPCSCDDGYPALDLDAGLEPSPGLEDPLLD 420
DB 361 SAYSEERDRPYGLVSIIDTVTVLDAEGCTWPCSCDDGYPALDLDAGLEPSPGLEDPLLD 420

QY 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSSEAGS 480
DB 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSSEAGS 480

QY 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLROWVIPPPLSSPGQAS 538
DB 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLROWVIPPPLSSPGQAS 538

RESULT 3
PCT-US02-29839-2
; Sequence 2, Application PC/TUS0229839
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Methods and Composition for Modulating Interleukin-21 Receptor Ac
; FILE REFERENCE: G15320-PCT-P2
; CURRENT APPLICATION NUMBER: PCT/US02/29839
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 09/972,218
; PRIOR FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Human
PCT-US02-29839-2

Query Match      100.0%; Score 2958; DB 1; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-236;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGWAAPLLLLLLOGGCGCPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60
DB 1 MPRGWAAPLLLLLLOGGCGCPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60

QY 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120
DB 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120

QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLOYELOYNRNGDPWAVSPRRKLIISVDS 180
DB 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLOYELOYNRNGDPWAVSPRRKLIISVDS 180

QY 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240
DB 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240

QY 241 LLLLVIVIPAFWSLTKTHPLWRLWKIWA VSPERFFMPLYKGCSDGPKKWWGAPFTGSS 300
DB 241 LLLLVIVIPAFWSLTKTHPLWRLWKIWA VSPERFFMPLYKGCSDGPKKWWGAPFTGSS 300

QY 301 LELGWPSPVSTLEVYSCHPPRSPAKRLQLTELQEPAAELVESDGVKPKSPFWPTAQNSSG 360
DB 301 LELGWPSPVSTLEVYSCHPPRSPAKRLQLTELQEPAAELVESDGVKPKSPFWPTAQNSSG 360

QY 361 SAYSEERDRPYGLVSIIDTVTVLDAEGCTWPCSCDDGYPALDLDAGLEPSPGLEDPLLD 420
DB 361 SAYSEERDRPYGLVSIIDTVTVLDAEGCTWPCSCDDGYPALDLDAGLEPSPGLEDPLLD 420

QY 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSSEAGS 480
DB 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSSEAGS 480

QY 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLROWVIPPPLSSPGQAS 538
DB 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLROWVIPPPLSSPGQAS 538

RESULT 2
PCT-US00-13687-2
; Sequence 2, Application PC/TUS0013687
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; TITLE OF INVENTION: Novel IL-9/IL-2 Receptor-Like Molecules
; FILE REFERENCE: 5800-17A-1
; CURRENT APPLICATION NUMBER: PCT/US00/13687
; CURRENT FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 09/313,913
; PRIOR FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens IL-2/IL-9 Receptor Like
PCT-US00-13687-2

Query Match      100.0%; Score 2958; DB 1; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-236;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGWAAPLLLLLLOGGCGCPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60
DB 1 MPRGWAAPLLLLLLOGGCGCPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60
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Db 241 LLLLVIVIPAFWSLKTPLWRLWKKIWAVSPERFPMPLYKCGSGDFKWKVGAFTGSS 300  
Qy 301 LELGWPSEVPSTLEVYCHPPSPAKRLQLTELQEPALVESDGVKPKSPFWPTAQNSSG 360  
Db 301 LELGWPSEVPSTLEVYCHPPSPAKRLQLTELQEPALVESDGVKPKSPFWPTAQNSSG 360  
Qy 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLEDPILLD 420  
Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLEDPILLD 420  
Qy 421 AGTTVLSGCGVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSSEAGS 480  
Db 421 AGTTVLSGCGVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSSEAGS 480  
Qy 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPQAS 538  
Db 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPQAS 538

RESULT 4  
PCT-US02-34502-16  
; Sequence 16, Application PC/TUS0234502  
; GENERAL INFORMATION:  
; APPLICANT: ZymoGenetics, Inc.  
; TITLE OF INVENTION: ZALPHALL LIGAND ANTAGONISTS  
; FILE REFERENCE: 01-37PC  
; CURRENT APPLICATION NUMBER: PCT/US02/34502  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR FILING DATE: 60/337,586  
; \* NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US02-34502-16

Query Match 100.0%; Score 2958; DB 1; Length 538;  
Best Local Similarity 100.0%; Pred. No. 1.5e-236;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGWAAPLLLLLOGGWGCPLVCYTDYLTQTVICILEMNNLHPSTLTLTWQDOYEELKD 60  
Db 1 MPRGWAAPLLLLLOGGWGCPLVCYTDYLTQTVICILEMNNLHPSTLTLTWQDOYEELKD 60

Qy 61 EATCSLHRSAHNATHATYTCHMDVHFHMADDIFSVNITDQSGNYSCGCSFLLAESIKP 120  
Db 61 EATCSLHRSAHNATHATYTCHMDVHFHMADDIFSVNITDQSGNYSCGCSFLLAESIKP 120

Qy 121 APPFNVTTFSGQYNIWSRSDYEDPAFYMLKGKQLQYELQYRNRGDPMWAVSPRRKLISVDS 180  
Db 121 APPFNVTTFSGQYNIWSRSDYEDPAFYMLKGKQLQYELQYRNRGDPMWAVSPRRKLISVDS 180

Qy 181 RSVALLEPRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIPTQSEELKEGWNPHILL 240  
Db 181 RSVALLEPRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIPTQSEELKEGWNPHILL 240

Qy 241 LLLLVIVIPAFWSLKTPLWRLWKKIWAVSPERFPMPLYKCGSGDFKWKVGAFTGSS 300  
Db 241 LLLLVIVIPAFWSLKTPLWRLWKKIWAVSPERFPMPLYKCGSGDFKWKVGAFTGSS 300

Qy 301 LELGWPSEVPSTLEVYCHPPSPAKRLQLTELQEPALVESDGVKPKSPFWPTAQNSSG 360  
Db 301 LELGWPSEVPSTLEVYCHPPSPAKRLQLTELQEPALVESDGVKPKSPFWPTAQNSSG 360

Qy 421 AGTTVLSGCGVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSSEAGS 480  
Db 421 AGTTVLSGCGVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSSEAGS 480

Qy 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPQAS 538  
Db 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPQAS 538

Db 421 AGTTVLSGCGVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSSEAGS 480  
Qy 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPQAS 538  
Db 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPQAS 538

RESULT 5  
PCT-US03-17808-6  
; Sequence 6, Application PC/TUS0317808  
; GENERAL INFORMATION:  
; APPLICANT: ZymoGenetics, Inc.  
; APPLICANT: Nelson, Andrew J.  
; APPLICANT: Hughes, Steven D.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Kindsvogel, Wayne R.  
; TITLE OF INVENTION: USE OF IL-21 IN CANCER AND  
; TITLE OF INVENTION: OTHER THERAPEUTIC APPLICATIONS  
; FILE REFERENCE: 02-11PC  
; CURRENT APPLICATION NUMBER: PCT/US03/17808  
; CURRENT FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: US 60/387,127  
; PRIOR FILING DATE: 2002-06-07  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US03-17808-6

Query Match 100.0%; Score 2958; DB 1; Length 538;  
Best Local Similarity 100.0%; Pred. No. 1.5e-236;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGWAAPLLLLLOGGWGCPLVCYTDYLTQTVICILEMNNLHPSTLTLTWQDOYEELKD 60  
Db 1 MPRGWAAPLLLLLOGGWGCPLVCYTDYLTQTVICILEMNNLHPSTLTLTWQDOYEELKD 60

Qy 61 EATCSLHRSAHNATHATYTCHMDVHFHMADDIFSVNITDQSGNYSCGCSFLLAESIKP 120  
Db 61 EATCSLHRSAHNATHATYTCHMDVHFHMADDIFSVNITDQSGNYSCGCSFLLAESIKP 120

Qy 121 APPFNVTTFSGQYNIWSRSDYEDPAFYMLKGKQLQYELQYRNRGDPMWAVSPRRKLISVDS 180  
Db 121 APPFNVTTFSGQYNIWSRSDYEDPAFYMLKGKQLQYELQYRNRGDPMWAVSPRRKLISVDS 180

Qy 181 RSVALLEPRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIPTQSEELKEGWNPHILL 240  
Db 181 RSVALLEPRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIPTQSEELKEGWNPHILL 240

Qy 241 LLLLVIVIPAFWSLKTPLWRLWKKIWAVSPERFPMPLYKCGSGDFKWKVGAFTGSS 300  
Db 241 LLLLVIVIPAFWSLKTPLWRLWKKIWAVSPERFPMPLYKCGSGDFKWKVGAFTGSS 300

Qy 301 LELGWPSEVPSTLEVYCHPPSPAKRLQLTELQEPALVESDGVKPKSPFWPTAQNSSG 360  
Db 301 LELGWPSEVPSTLEVYCHPPSPAKRLQLTELQEPALVESDGVKPKSPFWPTAQNSSG 360

Qy 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLEDPILLD 420  
Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLEDPILLD 420

Qy 421 AGTTVLSGCGVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSSEAGS 480  
Db 421 AGTTVLSGCGVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSSEAGS 480

Qy 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPQAS 538  
Db 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPQAS 538

RESULT 6

PCT-US03-21975-4  
; Sequence 4, Application PC/TUS0321975  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Grusby, Michael J  
; APPLICANT: Wurster, Andrea  
; APPLICANT: Young, Deborah  
; APPLICANT: Collins, Mary  
; APPLICANT: Whitters, Matthew  
; TITLE OF INVENTION: Methods and Compositions for Modulating T Helper (TH)  
; FILE REFERENCE: 22058-585-061  
; CURRENT APPLICATION NUMBER: PCT/US03/21975  
; CURRENT FILING DATE: 2003-07-15  
; PRIOR APPLICATION NUMBER: 60/396,160  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: 60/403,001  
; PRIOR FILING DATE: 2002-08-12  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US03-21975-4

Query Match 100.0%; Score 2958; DB 1; Length 538;  
Best Local Similarity 100.0%; Pred. No. 1.5e-236;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGWAAPLILLLQGGWCPDLVCYTDYLTQVICILEMNLHPSTLTLTWQOYEELKD 60  
Db 1 MPRGWAAPLILLLQGGWCPDLVCYTDYLTQVICILEMNLHPSTLTLTWQOYEELKD 60

Qy 61 EATSCSLHRSAHNATHATYTCMDVHFHMADDIFSNNITDQSGNYSQECGSFLAESIKP 120  
Db 61 EATSCSLHRSAHNATHATYTCMDVHFHMADDIFSNNITDQSGNYSQECGSFLAESIKP 120

Qy 121 APPFNVTFTSGQYNIWSRSDYEDPAFYMLKGKLOYELQYRNRGDPWAVSPRKLISVDS 180  
Db 121 APPFNVTFTSGQYNIWSRSDYEDPAFYMLKGKLOYELQYRNRGDPWAVSPRKLISVDS 180

Qy 181 RSVSLLEPRKDSYELQVRAGMPGSSYQGTWSEMSDPVIFQTQSEELKEGWNPHLL 240  
Db 181 RSVSLLEPRKDSYELQVRAGMPGSSYQGTWSEMSDPVIFQTQSEELKEGWNPHLL 240

Qy 241 LLLLVIVFIPAFWSLKTPLWRLWKIWA VSPERFMPYKGCSDGFKKWVGAPFTGSS 300  
Db 241 LLLLVIVFIPAFWSLKTPLWRLWKIWA VSPERFMPYKGCSDGFKKWVGAPFTGSS 300

Qy 301 LEIGPWSPEVPSTLEVYSCHPSPAKRLQTLQEPAEELVESDGVKPSFWPTAQN SGG 360  
Db 301 LEIGPWSPEVPSTLEVYSCHPSPAKRLQTLQEPAEELVESDGVKPSFWPTAQN SGG 360

Qy 361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDLADGLESPGLDPLLD 420  
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDLADGLESPGLDPLLD 420

Qy 421 AGTTVLSGCGVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGGVSESEAGS 480  
Db 421 AGTTVLSGCGVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGGVSESEAGS 480

Qy 481 PLAGLDMDTFDSGFVSDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPLSSPGPQAS 538  
Db 481 PLAGLDMDTFDSGFVSDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPLSSPGPQAS 538

RESULT 7  
PCT-US04-08833-6  
; Sequence 6, Application PC/TUS0408833  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF

PCT-US03-21975-4  
; Sequence 4, Application PC/TUS0321975  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Grusby, Michael J  
; APPLICANT: Wurster, Andrea  
; APPLICANT: Young, Deborah  
; APPLICANT: Collins, Mary  
; APPLICANT: Whitters, Matthew  
; TITLE OF INVENTION: Methods and Compositions for Modulating T Helper (TH)  
; FILE REFERENCE: 22058-585-061  
; CURRENT APPLICATION NUMBER: PCT/US03/21975  
; CURRENT FILING DATE: 2003-07-15  
; PRIOR APPLICATION NUMBER: 60/396,160  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: 60/403,001  
; PRIOR FILING DATE: 2002-08-12  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US03-21975-4

Query Match 100.0%; Score 2958; DB 1; Length 538;  
Best Local Similarity 100.0%; Pred. No. 1.5e-236;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGWAAPLILLLQGGWCPDLVCYTDYLTQVICILEMNLHPSTLTLTWQOYEELKD 60  
Db 1 MPRGWAAPLILLLQGGWCPDLVCYTDYLTQVICILEMNLHPSTLTLTWQOYEELKD 60

Qy 61 EATSCSLHRSAHNATHATYTCMDVHFHMADDIFSNNITDQSGNYSQECGSFLAESIKP 120  
Db 61 EATSCSLHRSAHNATHATYTCMDVHFHMADDIFSNNITDQSGNYSQECGSFLAESIKP 120

Qy 121 APPFNVTFTSGQYNIWSRSDYEDPAFYMLKGKLOYELQYRNRGDPWAVSPRKLISVDS 180  
Db 121 APPFNVTFTSGQYNIWSRSDYEDPAFYMLKGKLOYELQYRNRGDPWAVSPRKLISVDS 180

Qy 181 RSVSLLEPRKDSYELQVRAGMPGSSYQGTWSEMSDPVIFQTQSEELKEGWNPHLL 240  
Db 181 RSVSLLEPRKDSYELQVRAGMPGSSYQGTWSEMSDPVIFQTQSEELKEGWNPHLL 240

Qy 241 LLLLVIVFIPAFWSLKTPLWRLWKIWA VSPERFMPYKGCSDGFKKWVGAPFTGSS 300  
Db 241 LLLLVIVFIPAFWSLKTPLWRLWKIWA VSPERFMPYKGCSDGFKKWVGAPFTGSS 300

Qy 301 LEIGPWSPEVPSTLEVYSCHPSPAKRLQTLQEPAEELVESDGVKPSFWPTAQN SGG 360  
Db 301 LEIGPWSPEVPSTLEVYSCHPSPAKRLQTLQEPAEELVESDGVKPSFWPTAQN SGG 360

Qy 361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDLADGLESPGLDPLLD 420  
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDLADGLESPGLDPLLD 420

Qy 421 AGTTVLSGCGVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGGVSESEAGS 480  
Db 421 AGTTVLSGCGVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGGVSESEAGS 480

Qy 481 PLAGLDMDTFDSGFVSDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPLSSPGPQAS 538  
Db 481 PLAGLDMDTFDSGFVSDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPLSSPGPQAS 538

RESULT 8  
US-09-159-254-2  
; Sequence 2, Application US/09159254  
; GENERAL INFORMATION:  
; APPLICANT: Fresnell, Scott R.  
; APPLICANT: Conklin, Darrell C.  
; APPLICANT: Parrish, Julia E.  
; APPLICANT: Hammond, Angela K.  
; TITLE OF INVENTION: Cytokine receptor zalphail  
; FILE REFERENCE: 98-55X  
; CURRENT APPLICATION NUMBER: US/09/159,254  
; CURRENT FILING DATE: 1998-09-23  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Fast-Seq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-159-254-2

Query Match 100.0%; Score 2958; DB 15; Length 538;  
Best Local Similarity 100.0%; Pred. No. 1.5e-236;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MPRGWAAPLLLLLQGGWGPCDLYCYTDYLTQTVICILEMNNLHPSTLTTLTWQDQYEELKD 60
Db 1 MPRGWAAPLLLLLQGGWGPCDLYCYTDYLTQTVICILEMNNLHPSTLTTLTWQDQYEELKD 60
QY 61 EATCSLHRSAHNATHATYTTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP 120
Db 61 EATCSLHRSAHNATHATYTTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP 120
QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLYELQYRNRPDPAVSPRRKLISVDS 180
Db 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLYELQYRNRPDPAVSPRRKLISVDS 180
QY 181 RSVSLPLLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEBELKEGWNPHLLL 240
Db 181 RSVSLPLLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEBELKEGWNPHLLL 240
QY 241 LLLLVIPIPAFWSLKTPLWRLWKKIWAVSPERFFMPLYKGCSDGDFKKWVGAPFTGSS 300
Db 241 LLLLVIPIPAFWSLKTPLWRLWKKIWAVSPERFFMPLYKGCSDGDFKKWVGAPFTGSS 300
QY 301 LELGWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSGG 360
Db 301 LELGWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSGG 360
QY 361 SAYSEERDRPYGLVSDITVTVDAGPCTWPCSCDDGYPALDDAGLEPSPGLDPLLD 420
Db 361 SAYSEERDRPYGLVSDITVTVDAGPCTWPCSCDDGYPALDDAGLEPSPGLDPLLD 420
QY 421 AGTTVLSCGCVSAGSPGLGGLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSVSEAGS 480
Db 421 AGTTVLSCGCVSAGSPGLGGLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSVSEAGS 480
QY 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 538
Db 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 538
```

RESULT 9

US-09-264-908-2

; Sequence 2, Application US/09264908  
; GENERAL INFORMATION:  
; APPLICANT: Parrish, Julia E.  
; APPLICANT: Hammond, Angela K.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Gross, Jane A.  
; APPLICANT: Johnston, Janet V.  
; APPLICANT: Xu, Wen-feng  
; APPLICANT: Grant, Francis J.  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Kuijper, Joseph L.  
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND  
; FILE REFERENCE: 99-16X  
; CURRENT APPLICATION NUMBER: US/09/264,908  
; CURRENT FILING DATE: 1999-03-09  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-264-908-2

Query Match 100.0%; Score 2958; DB 16; Length 538;  
Best Local Similarity 100.0%; Pred. No. 1.5e-236;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MPRGWAAPLLLLLQGGWGPCDLYCYTDYLTQTVICILEMNNLHPSTLTTLTWQDQYEELKD 60
Db 1 MPRGWAAPLLLLLQGGWGPCDLYCYTDYLTQTVICILEMNNLHPSTLTTLTWQDQYEELKD 60
QY 61 EATCSLHRSAHNATHATYTTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP 120
Db 61 EATCSLHRSAHNATHATYTTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP 120
QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLYELQYRNRPDPAVSPRRKLISVDS 180
Db 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLYELQYRNRPDPAVSPRRKLISVDS 180
QY 181 RSVSLPLLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEBELKEGWNPHLLL 240
Db 181 RSVSLPLLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEBELKEGWNPHLLL 240
QY 241 LLLLVIPIPAFWSLKTPLWRLWKKIWAVSPERFFMPLYKGCSDGDFKKWVGAPFTGSS 300
Db 241 LLLLVIPIPAFWSLKTPLWRLWKKIWAVSPERFFMPLYKGCSDGDFKKWVGAPFTGSS 300
QY 301 LELGWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSGG 360
Db 301 LELGWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSGG 360
QY 361 SAYSEERDRPYGLVSDITVTVDAGPCTWPCSCDDGYPALDDAGLEPSPGLDPLLD 420
Db 361 SAYSEERDRPYGLVSDITVTVDAGPCTWPCSCDDGYPALDDAGLEPSPGLDPLLD 420
QY 421 AGTTVLSCGCVSAGSPGLGGLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSVSEAGS 480
Db 421 AGTTVLSCGCVSAGSPGLGGLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSVSEAGS 480
QY 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 538
Db 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 538
```

RESULT 10

US-09-265-117-2  
; Sequence 2, Application US/09265117  
; GENERAL INFORMATION:  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Conklin, Darrell C.  
; APPLICANT: Parrish, Julia E.  
; APPLICANT: Hammond, Angela K.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZALPHA11  
; FILE REFERENCE: 98-55X2  
; CURRENT APPLICATION NUMBER: US/09/265,117  
; CURRENT FILING DATE: 1999-03-09  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-265-117-2

Query Match 100.0%; Score 2958; DB 16; Length 538;  
Best Local Similarity 100.0%; Pred. No. 1.5e-236;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MPRGWAAPLLLLLQGGWGPCDLYCYTDYLTQTVICILEMNNLHPSTLTTLTWQDQYEELKD 60
Db 1 MPRGWAAPLLLLLQGGWGPCDLYCYTDYLTQTVICILEMNNLHPSTLTTLTWQDQYEELKD 60
QY 61 EATCSLHRSAHNATHATYTTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP 120
Db 61 EATCSLHRSAHNATHATYTTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP 120
QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLYELQYRNRPDPAVSPRRKLISVDS 180
Db 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLYELQYRNRPDPAVSPRRKLISVDS 180
```

QY 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVI FQTQSEELKEGWNPHLLL 240  
DB 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVI FQTQSEELKEGWNPHLLL 240  
QY 241 LLLLVIPIAFWSLKTHTPLWRLWKIWAIVSPERFMPLYKGCSDGPKWVGAPFTGSS 300  
DB 241 LLLLVIPIAFWSLKTHTPLWRLWKIWAIVSPERFMPLYKGCSDGPKWVGAPFTGSS 300  
QY 301 LELGWSPEVSTLEVISCHPSPRSAPKRLQTLQELQPAELVESDGVKPSFWPTAQNSSG 360  
DB 301 LELGWSPEVSTLEVISCHPSPRSAPKRLQTLQELQPAELVESDGVKPSFWPTAQNSSG 360  
QY 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLD 420  
DB 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLD 420  
QY 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
DB 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
QY 481 PLAGLDMDTFSGFGVSGDCSPVECDFTSPGDEGPPRSYLRQWVVI PPLSSPGQAS 538  
DB 481 PLAGLDMDTFSGFGVSGDCSPVECDFTSPGDEGPPRSYLRQWVVI PPLSSPGQAS 538

## RESULT 11

US-09-313-913-2  
; Sequence 2, Application US/09313913  
; GENERAL INFORMATION:  
; APPLICANT: Hodge, Martin R.  
; TITLE OF INVENTION: Novel IL-9/IL-2 Receptor-Like Molecules and Uses  
; FILE REFERENCE: 035800/173733 (5800-17)  
; CURRENT APPLICATION NUMBER: US/09/313,913  
; CURRENT FILING DATE: 1999-05-18  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-313-913-2

Query Match 100.0%; Score 2958; DB 17; Length 538;  
Best Local Similarity 100.0%; Pred. No. 1.5e-236;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MPRGWAAPLLLLLQGGWGPCDVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60  
DB 1 MPRGWAAPLLLLLQGGWGPCDVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60  
QY 61 EATCSLHRSAINATHATYTCHMDVHFHMADDIFSUNITDQSGNYSCGSGFLAESIKP 120  
DB 61 EATCSLHRSAINATHATYTCHMDVHFHMADDIFSUNITDQSGNYSCGSGFLAESIKP 120  
QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYLKGLQYELQYRNRGDPWAVSPRKLISYDS 180  
DB 121 APPFNVTTFSGQYNISWRSDYEDPAFYLKGLQYELQYRNRGDPWAVSPRKLISYDS 180  
QY 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVI FQTQSEELKEGWNPHLLL 240  
DB 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVI FQTQSEELKEGWNPHLLL 240  
QY 241 LLLLVIPIAFWSLKTHTPLWRLWKIWAIVSPERFMPLYKGCSDGPKWVGAPFTGSS 300  
DB 241 LLLLVIPIAFWSLKTHTPLWRLWKIWAIVSPERFMPLYKGCSDGPKWVGAPFTGSS 300  
QY 301 LELGWSPEVSTLEVISCHPSPRSAPKRLQTLQELQPAELVESDGVKPSFWPTAQNSSG 360  
DB 301 LELGWSPEVSTLEVISCHPSPRSAPKRLQTLQELQPAELVESDGVKPSFWPTAQNSSG 360  
QY 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLD 420  
DB 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLD 420  
QY 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
DB 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
QY 481 PLAGLDMDTFSGFGVSGDCSPVECDFTSPGDEGPPRSYLRQWVVI PPLSSPGQAS 538  
DB 481 PLAGLDMDTFSGFGVSGDCSPVECDFTSPGDEGPPRSYLRQWVVI PPLSSPGQAS 538

DB 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLD 420  
QY 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
DB 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
QY 481 PLAGLDMDTFSGFGVSGDCSPVECDFTSPGDEGPPRSYLRQWVVI PPLSSPGQAS 538  
DB 481 PLAGLDMDTFSGFGVSGDCSPVECDFTSPGDEGPPRSYLRQWVVI PPLSSPGQAS 538

## RESULT 12

US-09-347-930-2  
; Sequence 2, Application US/09347930  
; GENERAL INFORMATION:  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Conklin, Darrell C.  
; APPLICANT: Parrish, Julia E.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Raymond, Fenella C.  
; APPLICANT: Hammond, Angela K.  
; APPLICANT: Gross, Jane A.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL  
; FILE REFERENCE: 98-55X3  
; CURRENT APPLICATION NUMBER: US/09/347,930  
; CURRENT FILING DATE: 1999-07-06  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-347-930-2

Query Match 100.0%; Score 2958; DB 17; Length 538;  
Best Local Similarity 100.0%; Pred. No. 1.5e-236;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MPRGWAAPLLLLLQGGWGPCDVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60  
DB 1 MPRGWAAPLLLLLQGGWGPCDVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60  
QY 61 EATCSLHRSAINATHATYTCHMDVHFHMADDIFSUNITDQSGNYSCGSGFLAESIKP 120  
DB 61 EATCSLHRSAINATHATYTCHMDVHFHMADDIFSUNITDQSGNYSCGSGFLAESIKP 120  
QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYLKGLQYELQYRNRGDPWAVSPRKLISYDS 180  
DB 121 APPFNVTTFSGQYNISWRSDYEDPAFYLKGLQYELQYRNRGDPWAVSPRKLISYDS 180  
QY 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVI FQTQSEELKEGWNPHLLL 240  
DB 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVI FQTQSEELKEGWNPHLLL 240  
QY 241 LLLLVIPIAFWSLKTHTPLWRLWKIWAIVSPERFMPLYKGCSDGPKWVGAPFTGSS 300  
DB 241 LLLLVIPIAFWSLKTHTPLWRLWKIWAIVSPERFMPLYKGCSDGPKWVGAPFTGSS 300  
QY 301 LELGWSPEVSTLEVISCHPSPRSAPKRLQTLQELQPAELVESDGVKPSFWPTAQNSSG 360  
DB 301 LELGWSPEVSTLEVISCHPSPRSAPKRLQTLQELQPAELVESDGVKPSFWPTAQNSSG 360  
QY 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLD 420  
DB 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLD 420  
QY 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
DB 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480  
QY 481 PLAGLDMDTFSGFGVSGDCSPVECDFTSPGDEGPPRSYLRQWVVI PPLSSPGQAS 538  
DB 481 PLAGLDMDTFSGFGVSGDCSPVECDFTSPGDEGPPRSYLRQWVVI PPLSSPGQAS 538

## RESULT 13

US-09-543-320-2  
; Sequence 2, Application US/09543320  
; GENERAL INFORMATION:  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Brandt, Cameron S.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS  
; FILE REFERENCE: 00-22X  
; CURRENT APPLICATION NUMBER: US/09/543,320  
; CURRENT FILING DATE: 2000-04-05  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-543-320-2

Query Match 100.0%; Score 2958; DB 19; Length 538;  
Best Local Similarity 100.0%; Pred. No. 1.5e-236;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MPRGWAAPLLLLLLQGGWGPCDLYCYTYDYLQTVICILEMNLHPSTLTLTWQDQYEELKD 60  
DB 1 MPRGWAAPLLLLLLQGGWGPCDLYCYTYDYLQTVICILEMNLHPSTLTLTWQDQYEELKD 60  
QY 61 EATCSLHRSAHNATHATTCHMDVHFHMADDIFSVNITDQSGNYSQECGSLLAESTKP 120  
DB 61 EATCSLHRSAHNATHATTCHMDVHFHMADDIFSVNITDQSGNYSQECGSLLAESTKP 120  
QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKQLQYELQYRNRPWAVSPRKLISVDS 180  
DB 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKQLQYELQYRNRPWAVSPRKLISVDS 180  
QY 181 RVSLLPLLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVIQTQSEBELKEGWNPHLLL 240  
DB 181 RVSLLPLLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVIQTQSEBELKEGWNPHLLL 240  
QY 241 LLLLVIVIPAFWSLKTHTPLRLMKKIWAVSPERFPMPLKYGCSGDPKKWVGAPFTGSS 300  
DB 241 LLLLVIVIPAFWSLKTHTPLRLMKKIWAVSPERFPMPLKYGCSGDPKKWVGAPFTGSS 300  
QY 301 LELGWSPEVSTLEVYSCHPSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSSG 360  
DB 301 LELGWSPEVSTLEVYSCHPSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSSG 360  
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLADGLEPSPGLDPLLD 420  
DB 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLADGLEPSPGLDPLLD 420  
QY 421 AGTTVLSGCVSAGSPGLGGPLGSLLDRLKPLADGEDWAGGLPWGGRSPGVSSSEAGS 480  
DB 421 AGTTVLSGCVSAGSPGLGGPLGSLLDRLKPLADGEDWAGGLPWGGRSPGVSSSEAGS 480  
QY 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538  
DB 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538

## RESULT 14

US-09-560-766-2  
; Sequence 2, Application US/09560766  
; GENERAL INFORMATION:  
; APPLICANT: Donaldson, Debra  
; APPLICANT: Unger, Michelle  
; TITLE OF INVENTION: MU-1 RECEPTOR  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive

CITY: Cambridge  
STATE: MA  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/560,766  
FILING DATE:  
CLASSIFICATION:  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/560,766  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A  
REGISTRATION NUMBER: 32,724  
REFERENCE/DOCKET NUMBER: G15320  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-498-8224  
TELEFAX: 617-876-5851  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 538 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-560-766-2

Query Match 100.0%; Score 2958; DB 19; Length 538;  
Best Local Similarity 100.0%; Pred. No. 1.5e-236;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MPRGWAAPLLLLLLQGGWGPCDLYCYTYDYLQTVICILEMNLHPSTLTLTWQDQYEELKD 60  
DB 1 MPRGWAAPLLLLLLQGGWGPCDLYCYTYDYLQTVICILEMNLHPSTLTLTWQDQYEELKD 60  
QY 61 EATCSLHRSAHNATHATTCHMDVHFHMADDIFSVNITDQSGNYSQECGSLLAESTKP 120  
DB 61 EATCSLHRSAHNATHATTCHMDVHFHMADDIFSVNITDQSGNYSQECGSLLAESTKP 120  
QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKQLQYELQYRNRPWAVSPRKLISVDS 180  
DB 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKQLQYELQYRNRPWAVSPRKLISVDS 180  
QY 181 RVSLLPLLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVIQTQSEBELKEGWNPHLLL 240  
DB 181 RVSLLPLLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVIQTQSEBELKEGWNPHLLL 240  
QY 241 LLLLVIVIPAFWSLKTHTPLRLMKKIWAVSPERFPMPLKYGCSGDPKKWVGAPFTGSS 300  
DB 241 LLLLVIVIPAFWSLKTHTPLRLMKKIWAVSPERFPMPLKYGCSGDPKKWVGAPFTGSS 300  
QY 301 LELGWSPEVSTLEVYSCHPSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSSG 360  
DB 301 LELGWSPEVSTLEVYSCHPSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSSG 360  
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLADGLEPSPGLDPLLD 420  
DB 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLADGLEPSPGLDPLLD 420  
QY 421 AGTTVLSGCVSAGSPGLGGPLGSLLDRLKPLADGEDWAGGLPWGGRSPGVSSSEAGS 480  
DB 421 AGTTVLSGCVSAGSPGLGGPLGSLLDRLKPLADGEDWAGGLPWGGRSPGVSSSEAGS 480  
QY 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538  
DB 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538

## RESULT 15

US-09-569-384-2  
; Sequence 2, Application US/09569384  
; GENERAL INFORMATION:  
; APPLICANT: Donaldson, Deborah  
; APPLICANT: Unger, Michelle  
; APPLICANT: Collins, Mary  
; APPLICANT: Whitters, Matthew J.  
; APPLICANT: Lowe, Leslie  
; APPLICANT: Young, Deborah A.  
; TITLE OF INVENTION: MU-1, MEMBER OF THE CYTOKINE RECEPTOR FAMILY  
; FILE REFERENCE: GFN-5230CP  
; CURRENT APPLICATION NUMBER: US/09/569.384  
; CURRENT FILING DATE: 2000-05-11  
; PRIOR APPLICATION NUMBER: 09/040,005  
; PRIOR FILING DATE: 1998-03-17  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-569-384-2

	Query Match	100.0%;	Score 2958;	DB 19;	Length 538;
Best Local Similarity	100.0%;	Pred. No. 1.5e-236;			
Matches 538;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	MPRGWAAPLLLLLLGGGCGCDPLVCYTDYLOTVICILEMNNLHPSTLTLTWQDQYEELKD	60		
Db	1	MPRGWAAPLLLLLLGGGCGCDPLVCYTDYLOTVICILEMNNLHPSTLTLTWQDQYEELKD	60		
QY	61	EATCSLHRSAHNATHYTCCHMDVHFEMADDIFSVNITDQSGNYSQECGSFLAESIKP	120		
Db	61	EATCSLHRSAHNATHYTCCHMDVHFEMADDIFSVNITDQSGNYSQECGSFLAESIKP	120		
QY	121	APPFNVTVTFSGQYNISNRSDYEDPAFYMLKGKQLQYELQYRNRGDPMAVSPRKLISYDS	180		
Db	121	APPFNVTVTFSGQYNISNRSDYEDPAFYMLKGKQLQYELQYRNRGDPMAVSPRKLISYDS	180		
QY	181	RSVSLPLLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLLL	240		
Db	181	RSVSLPLLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLLL	240		
QY	241	LLLLVIVIFAPFWSLKTPLMLWKIWAVPSPERFPMPLKGCSDGPKKWWGAPFTGSS	300		
Db	241	LLLLVIVIFAPFWSLKTPLMLWKIWAVPSPERFPMPLKGCSDGPKKWWGAPFTGSS	300		
QY	301	LELGPSPSPVSTLEVISCHPSPSPAKRIQLTELQEPALVESDGVKPSFWPTAQNSSG	360		
Db	301	LELGPSPSPVSTLEVISCHPSPSPAKRIQLTELQEPALVESDGVKPSFWPTAQNSSG	360		
QY	361	SAYSEERDRPYGLVSDITVTLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLDPLLD	420		
Db	361	SAYSEERDRPYGLVSDITVTLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLDPLLD	420		
QY	421	AGTTVLSCGCVSAGSPGLGSLDLRLKPLADGEDWAGLPMGGSPGCVSESEAGS	480		
Db	421	AGTTVLSCGCVSAGSPGLGSLDLRLKPLADGEDWAGLPMGGSPGCVSESEAGS	480		
QY	481	PLAGLDMDTFDSGFGVSGDCSSPVECDFTSPGDEGPPRSYLROWVIPPPLSSPGFQAS	538		
Db	481	PLAGLDMDTFDSGFGVSGDCSSPVECDFTSPGDEGPPRSYLROWVIPPPLSSPGFQAS	538		

Search completed: July 9, 2005, 11:56:42  
Job time : 478 secs